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Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
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                                                                                                                                                                                                                                                                                                                       Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                               799.5
768
765
759
                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length: 2000000000
100.0
88.1
88.0
70.6
56.9
54.6
54.4
42.7
42.7
                                                                                                                                                                                                                                                                                                                       Match
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2: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1981.DAT: *
3: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1981.DAT: *
3: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1981.DAT: *
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5: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1981.DAT: *
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10: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1989.DAT: *
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27: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1999.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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        100%
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                                                                                                                                                                    AAM24188
AAE04897
  AAM41845
AAE06612
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AAB47276
                                                        AAB19406
AAE10332
                                                                                                              AAM40059
                                                                                                                                        AAB47275
                                                                                                                                                                                                                          ABB11732
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                                                                                       Human polypeptide
Amino acid sequenc
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                                                                                                                                                                    Human transporter
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n secreted pro
n EST encoded
        protein hav:
                                  polypeptide
                                                           transporter
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267 231.5 228	295 289.5 286.5	296.5 296.5	307.5	308	324.5	344	344	3//	344	344	~	362.5	~·	373	386.5	390.5	N	436.5	•	8	458.5	458.5	472	588.5	90	592
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AAB12131 ABG27003 ABB60174	AAB08824 ABG26897 AAM96463	AABU8823 ABB12030	AAB47272	AAB49401 AAB47273	AAY51249	AAM38292	AAM21954	AAM78066	MA5378	ABB44330	AAW44196	AAY92903	AAW44195	AAU33066	AAB47274	AAY92902	ABG26899	AAB36553	AAW88488	AAW88489	AAB47271	AAY44278	AAU32379	AAE06571	AAE10336	AAB69091
Hydrophobic domain Novel human diagno Drosophila melanog	Novel human diagno Human reproductive	Human liver-specif	3 •	hOAT2B. Homo sapi	ver anion				ain ex	Protein #9189 enco	#1100K	The state of	Mouse osteoclast t	Novel human secret	. Hom	cerebr	Novel human diagno	Mouse organic anio	Rat organic anion	Human organic anio	hOAT1. Homo sapie	organic	numan se	n proce	Human transporter	_

ALIGNMENTS

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RESULT
AAY52386
HP02000; transmembrane domain; liver; expression; homology; organic cation transporter; drug excretion; antibody; assay reagent; diagnostic marker; primer; probe; antisense; gene therapy;
                                                                                                                                                                                                                                                     09-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                         AAY52386 standard; Protein; 268 AA
                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                   agonist; antagonist; ligand; therapeutic
                                                                                                                                                                                                                                 Human transmembrane protein HP02000.
                                                                                                                                                                                                                                                                       AAY52386;
                                                                                                                               04-NOV-1999.
                                                                                                                                                  W09955862-A2
                                                                                           28-APR-1998;
                                                                                                             27-APR-1999;
                                                               (SAGA ) SAGAMI CHEM RES CENT. (PROT-) PROTEGENE INC.
                                                                                                                                                                                                                                                                                                          Ъ
                                                                                            98JP-0119395.
                                                                                                              99WO-JP02226.
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Human proteins with transmembrane domains, involved in control of cell

WPI; 2000-023358/02. N-PSDB; AAZ38316, AAZ38317.

Kato S, Kimura T;

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Best Local Similarity
                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; organic anion transporter; hOAT; liver; kidney;
membrane protein; transport; organic anion; splice variant.
                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                   Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists which are potentially useful therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 RICILVELRKKISRKRHKNDCYTKVTKF 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLERNDSMRK 240
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                                                                                                                                                                                                                                                      /note=
289
                                                                /note= "PKC phosphorylation site"
526
                                                                                                                                                        /note= "PKC phosphorylation site"
345
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1406; DB 21; 100.0%; Pred. No. 1.2e-143;
"PKC phosphorylation site"
                                                                                                                                                                                                                                                                                   "PKC phosphorylation site"
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Best Local Similarity
ABB11732 standard; peptide; 391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAB47271-76 represent human organic anion transporter (hOAT) polypeptides. hOAT polypeptides are preferentially expressed in the liver and kidneys of humans. OAT's are membrane proteins that facilitate the transport of organic anions across the cell membrane. The mechanism of transport is thought to be a secondary or tertiary active transport involving exchange active transport involving exchanges for another organic anion. HoAT2A and hOAT2B are thought to be splice variants as they are encoding them, may be used in the prevention, treatment and diagnosis
                                                              of diseases associated with inappropriate hOAT expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human organic anion transporter polypeptides, useful in gene therapy procedures - \,
                                                                                                                 241 lsigqiilgglayvfrdwqtlhvvasvpflgllllqrwlvesarwliitnkldeglkalr 300
                                                                                                                                                                                181
                                                                                                                                                                                                                            Claim 2; Fig 6; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-367057/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-2000; 2000WO-US18980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (META-) METABASIS THERAPEUTICS INC.
                                                                                                                                                                                                                                                                               1 MAFFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                               w
                                                                                                                                                                      lqlaitdtcaafaptfpvycvlrflagfssmiiisnnslpitewirpnskalvvilssga 240
                                                                                                                                                                                                                                                                                                                                                                                                  249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC85824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0143771
                                                                                                                                                                                                                                                                                                                                                                                                          88.1%;
69.7%;
                                                                                                                                     -----RULVESARWLIITNKLDEGLKALR 192
                                                                                                                                                                                                                                                                                                                                                                                            Score 1238; DB 22;
Pred. No. 5.2e-125;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 541;
                                                                                                                                                                                                                                                                                                                                                                                            Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Human secreted protein homologue, SEQ ID NO:2102

11-JAN-2002 (first entry)

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myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antilucer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
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Homo sapiens.

09-AUG-2001

05-FEB-2001; 2001WO-US03800

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

(HYSE-) HYSEQ INC.

Liu C, Drmanac

N-PSDB; ABA08976 2001-457740/49

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer – $\,$

Claim 20; Page 235-236; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The CC invention also relates to vectors and recombinant host cells comprising a CC invention also relates to vectors and recombinant host cells comprising a CC nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides CC or polypeptides in a sample, and methods of identifying compounds which CC bind to polypeptides of the invention. Although novel, many of the CC polypeptides of the invention have homology to known proteins, thereby CC quing an insight into their probable biological activities, and hence CC potential therapeutic applications. The polypeptides of the invention may CC have various activities; including cytokine, cell proliferation or cell CC differential therapeutic applications of the invention ccll CC differential to activities; stem cell growth factor activity; cc haematopolesis regulatory activity; tissue growth activities; cremothation or chemokinetic activities; haemastatic, thrombotic or chemokinetic activities; haemastatic, thrombotic or may be thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders, chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides also be used in the diagnosis of the above conditions, and in

> 밁 Ş B QΥ 맑 Ş 밁 δÃ 밁 δÃ δÃ Matches 250; Best Local screening techniques. The present sequence represents a novel human polypeptide of the invention. 327 267 121 VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSD-------61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120 1 MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS kvartngiknaeetlnievvrstmqeeldaaqtkttvwdlfrnpsmrkricilvflrkk 385 KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFLRKK 251 lnigqiilgglayvfrdwqtlhvvasvpffvffllsrwlvesarwliitnkldeglkalr 326 lqlaitdtcaafaptfpvycvlrflagfssmiiisnnslpitewirpnskalvvilssga 266 -----RWLVESARWLIITNKLDEGLKALR 192 Similarity 391 AA; Conservative 88.0%; 0; Mismatches Score 1237; DB 22; Pred. No. 4.1e-125; Length Indels 108; Gaps 86 60 168

AAM24188 AAM24188 standard; Protein; 4

213

12-OCT-2001 (first entry)

Human EST encoded protein SEQ ID NO: 1713.

Human; sheep; piq; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.

Homo sapiens

WO200154477-A2

25-JAN-2001; 2001WO-US02687

25-JAN-2000; 2000US-0491404. 17-JUL-2000; 2000US-0617746. 03-AUG-2000; 2000US-0631451. 15-SEP-2000; 2000US-0663870.

(HYSE-) HYSEQ INC

Drmanac RA, Liu C, Zhou P, ou P, Qian Zhang J, V Werhman XB, Wang Z, Chen R, Asundi V;

N-PSDB; AAH98847. 2001-476164/51.

antibodies and research use Isolated polypeptide for treatment of diseases, diagnostics, raising

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Best Local
                                                                                                                                                                                                Human; transporter and ion channel-10; TRICH-10; cystic fibrosis; mood; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; vaccine; arrhythmia; Pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke; Huntington's disease; mental disorder; cerebral neoplasm; allergy; muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease; mental disorder; schizophrenia; polymyositis; dermatomyositis; diabetes mellitus; immunological disorder; psoriasis; rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease; mallabsorption syndrome; hypercholesterolaemia; cancer.
                               WO200146258-A2
                                                                             Domain
                                                                                                                                                                                  Homo sapiens.
                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                               Human transporter and ion channel-10 (TRICH-10) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE04897 standard; Protein; 553 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ngiknae 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 NGIKNAE 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pldsnlrpekcrrfvhpqwqllhlngtihstseadtepcvdgwvydqsyfpstivtkwdl 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLDSNLRPEKCRREVHPQWQLLHLNGTIHSTSBADTEPCVDGWVYDQSYEPSTIVTKWDL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                  Location/Qualifiers 204..222
                                                           /label=
                                                                                   /label= Transmembrane_domain
                                                                                                                   abel= Transmembrane_domain
                                                                                                      .493
                                                                           519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.6%; Score 993; DB 22; Length 213; 100.0%; Pred. No. 4.4e-99;
                                                        Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is transporter and ion channel-10 (TRICH-10) CC protein. TRICH is used as vaccine. TRICH is useful for treating a disease CC or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, CC cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth CC disease, Duchenne muscular dystrophy, angina and hypertension, enurological disorders including Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, ischaemic cerebrovascular CC disease, stroke, cerebral neoplasms, Plok's disease, Huntington's CC disease and parkinson's disease, demyelinating diseases, Huntington's CC disease and parkinson's disease, demyelinating diseases, mental disorders comuscle disorder including cardiomyopathy, myocarditis, polymyositis, communicated disorder including AlDS, adult respiratory distress syndrome (ARDS), allergies, CC anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary CC artery stenosis, Grave's disease, Cushing's disease, Addison's disease, Solving and viral, bacterial, fungal, heminthic and protozoal confections. TRICH DNA is useful in gene therapy and in diagnostic
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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21-JAN-2000;
28-JAN-2000;
02-FEB-2000;
                                                                                                       121
                                                                                                                Claim 1; Page 122-123; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human transporter and ion channel proteins useful for treating and preventing transport, neurological, muscle and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-418042/44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1999;
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                                                                                                                                                            61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-FEB-2000;
                                                                                                                                                                                                                            l mafqdllghagdlwrfqilqtvflsifavatylhf\mathtt{mlenftafipghrcwvhildndtvs} 60
                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                           1 MAFEELLSQVGGLGRFQMLHLVFTLPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS
                            \tt lqvaivgtcaalaptfliycslrflsgiaamslitntimliaewathrfqamgitlgmcp
                                                                                           vydrisfsstivtewdlvcdsqs1tsvakfvfmagmmvggilgghlsdrfgrrfvlrwcy 180
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Khan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD09561.
                                                                                                                                                                                                                                                                                                                                                                                553 AA;
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2000US-0176083.
2000US-0177332.
2000US-0178572.
2000US-0179758.
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                                                                                                                                                                                                                                                                                                                 56.98;
44.78;
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Yue H, Nguyen DB,
                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                              Score 799.5; DB 22; Pred. No. 1.7e-77;
                                                                                                                                                                                                                                                                                                Mismatches
-WLVESARWLIITNKLDEGLKALR
                                                                                                                                                                                                                                                                                             49; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang J,
                                                                                                                                                                                                                                                                                                                             Length 553;
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Gandhi AR;
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 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; organic anion transporter; hOAT; liver; kidney;
membrane protein; transport; organic anion; splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 KVARTNGIKNAEETLNIEVVRSTMOEELDAAQ-TKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 sgiafmtlaglafairdwhilqlvvsvpyfvifltsswllesarwliinnkpeeglkelr 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                          The sequences given in AABA7271-76 represent human organic anion transporter (hOAT) polypeptides. hOAT polypeptides are preferentially expressed in the liver and kidneys of humans. OAT's are membrane proteins that facilitate the transport of organic anions across the proteins that facilitate the transport of organic anions across the cell membrane. The mechanism of transport is thought to be a secondary cell membrane transport involving exchange of another organic anion. hoAT2A and hoAT2B are thought to be splice variants as they are identical except at the C-terminal end. hoAT proteins and the DNA encoding them, may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate hoAT expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-2000; 2000WO-US18980.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (META-) METABASIS THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human organic anion transporter polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC85823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 5; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful in gene therapy procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-367057/38.
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
 121 VYDQSYFPSTI-VTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------ 169
                             61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSBADTEPCVDGW 120
                                                                                                                                                                    Local Similarity
                                                                                         1 mafqdilghagdiwrfqilqtvflsifavatylhfmlenftafipghrcwvhildndtvs 60
                                                                                                                      1 MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                                                                                                                                                   554 AA;
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0143771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                       54.6%; Score 768; DB 22; Length 554; 43.7%; Pred. No. 4.4e-74;
                                                                                                                                                           40; Mismatches
                                                                                                                                                                Indels 110; Gaps
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AAM40059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-06523450.

14-SEP-2000; 2000US-0662191.

14-SEP-2000; 2000US-06621936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; alzheimer syndrome; chemotactic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM40059 standard; Protein; 341 AA.
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121 vydrisfsstigdlkwdlvcdsqsltsvakfvfmagmmlggilgvhlsdrfgrsfvlrwc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 3204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM40059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 RKVARTNGIKNAEETLNIEVVRSTMOEELDAAQ-TKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 -----WLVESARWLIITNKLDEGLKAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ylqvalvgtcaalaptfliycsvrflsgiaamsfitntlmllaewathrfqamgitlgmc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 psgiafmtlaglafairdwhilqlvvsvpyfvifltsswilesarwliinnkpeegikel 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukaemia.
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the uncoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide in gene therapy. A composition containing a polypeptide or polynucleotide in gene therapy and seripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system disease, such as localised neuropathies and central nervous system disease, such as localised neuropathies and central nervous system disease, amyotrophic Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-2000; 2000US-0727344
                                                                                                                                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                 Example 5; SEQ ID NO 3204; 10078pp; English.
                                                                                                                                                                                                                                                                                                  N-PSDB; AAI59215
                                                                                                                                                                                                                                                                                                                        WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                           Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                              Wang Z,
                                                                                                                                                                                                                                                                                                                                                                Zhou P,
                                                                                                                                                                                                                                                                                                                                                             Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                          Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                            Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                   Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                 Wang D;
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ACCOMMENS OF STREET STR
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AAB19406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         γΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δõ
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N-PSDB; AAC61892
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                            WPI; 2000-665133/64.
                                                                                             Garcia PD;
                                                                                                                                                                                                                                             09-APR-1999;
                                                                                                                                                      (CHIR ) CHIRON CORP
                                                                                                                                                                                                                 20-AUG-1999;
                                                                                                                                                                                                                                                                                         10-APR-2000; 2000WO-US09555.
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200061755-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein; platelet disorder; stem cell disorder; osteoporosis; osteoarthiitis; burn; incision; ulcer; periodontal disease; neuropathy; nervous system disease; bone growth; cosmetic plastic surgery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone marrow transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a human secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB19406 standard; Protein; 339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 kaahrsgmknardtltleilkstmkkeleaagkk 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      utilisation of the activities such as: Immune system suppression, Activity/Inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and c.N.S disorders.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 sgiafmtlaglafairdwhilqlvvsvpyfvifltsswllesarwliinnkpeeglkelr 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 lqvaivgtcaalaptfliycslrflsgiaamslitntimliaewathrfqamgitlgmcp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protection; gut regeneration; fibrosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\bf 1} \ {\tt mafqdllghagdlwrfqilqtvflsifavatylhfmlenftafipghrcwvhildndtvs} \ \ {\bf 60}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                     99US-0150054.
                                                                                                                                                                                                                                       99US-0128574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.4%; Score 765; DB 22; 45.5%; Pred. No. 4.5e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -------WLVESARWLIITNKLDEGLKALR 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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types which express the proteins. The polynucleotide molecules can be responses. The proteins and antibodies are useful in diagnosis and proteins. The proteins and antibodies are useful in diagnosis and proteins. The proteins are also useful for prevention or treatment of proteins are also useful for prevention or treatment of burns, incisions, ulcers, periodontal diseases, central and peripheral and to induce cartilage and/or bone growth in cosmetic plastic surgery. Treatment of lung or liver fibrosis, for stimulating blood cell treatment of lung or liver fibrosis, for stimulating blood cell of bone marrow transplantation patients.
    Sequence
                                                                                                                                                                                                                                                                                        AAB19393-B19407 represent secreted human proteins. The secreted proteins are useful in assays to determine their biological activities. The proteins can also be used as biomarkers to identify tissues or cell
                                                                                                                                                                                                                                                                                                                                                                                                                   Novel secreted human proteins useful for stimulating blood cell generation in patients receiving cancer chemotherapy, treating bone marrow transplantation patients and for healing fractured bones .
                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; Page 72; 74pp; English.
· 339 AA;
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                                                                                                                                                                                                                                                                                                                                                                                   Matches
301 kaahrsgmknardtltleilkstmkkeleaaqkkkt 336
                               193 KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTT 228
                                                        241 sgiafmtlaglafairdwhilqlvvsvpyfvifltsswilesarwliinnkpeeglkelr 300
                                                                                                                    181 lqvaivgtcaalaptfliycllrflsgiaamslitntimliaewathrfqamgitlgmcp
                                                                                                                                                                              121 vydrisfssaivtewdlvcdsqsltsvakfvfmagmmvggilgghlsdrfgrrfvlrwcy 180
                                                                                                                                                                                                 61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                     1 mafqdllghagdlwrfqilqtvflsifavatylhfmlenftafipghrcwvhildndtvs 60
                                                                                                                                                                                                                                                                                                                                    1 MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                      -----WLVESARWLIITNKLDEGLKALR 192
                                                                                                                                                                                                                                         dndtgalsqdallristpldsnmrpekcrrfvhpgwgllhlngtfpntsdadmepcvdgw 120
                                                                                                                                                                                                                                                                                                                                                                                     151;
                                                                                                                                                                                                                                                                                                                                                                                           h 54.0%;
Similarity 44.9%;
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                      Score 759; DB 2
Pred. No. 2e-73;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  DB_21; Length 339;
                                                                                                                                                                                                                                                                                                                                                                      44; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                   169
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AAE10332
10-DEC-2001 (first entry)
                                                      AAE10332 standard; Protein; 553
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Human transporter and ion channel-9 (TRICH-9) protein.

Human; transporter and ion channel; TRICH-9; therapy; akinesia; cardiant; neurological disorder; immune disorder; allergy; nootropic; dementia; AIDS; Acquired Immune Deficiency Syndrome; amyotrophic lateral sclerosis; cystic fibrosis; Alzheimer's disease; depression; epilepsy; scleroderma; cardiomyopathy; muscular dystrophy; Crohn's disease; multiple sclerosis; rheumatoid arthritis; cancer; anaemia; asthma; trauma; haemodialysis;

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25-FEB-2000; 2000US-0184866.
02-MAR-2000; 2000US-0187947.
09-MAR-2000; 2000US-0188333.
17-MAR-2000; 2000US-0190230.
17-MAR-2000; 2000US-0192077.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200162923-A2.
                                                                                                                                                                                    Matches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-FEB-2001; 2001WO-US05942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2000;
                                                                                                                                                                                                                                                                                                      The present sequence is human transporters and ion channels (FRICH-9) protein. The TRICH DNA, protein and their agonist and antagonists are useful in the diagnosis, treatment and prevention of transport disorders (akinesia, amyotrophic lateral sclerosis, cystic transport disorders (akinesia, amyotrophic lateral sclerosis, cystic fibrosis), neurological (Alzheimer's disease, dementia, depression, epilepsy), muscle (e.g. cardiomyopathy, Becker's muscular dystrophy) epilepsy), muscle (e.g. allergies, acquired immunodeficiency immunological disorders (e.g. allergies, acquired immunodeficiency syndrome (AIDS), Crohn's disease, rheumatoid arthritis, scleroderma, syndrome (AIDS), viral, bacterial, parasitic, protozoal and multiple sclerosis), viral, bacterial, parasitic, protozoal and helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis, helminthic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thirteen human transporters and ion channels (referred to as TRICH-1 to TRICH-13), useful in the diagnosis, treatment and prevention of transport (e.g. akinesia), neurological, muscle or immunological disorders (e.g. allergies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-582050/65.
N-PSDB; AAD17476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 114-115; 131pp; English.
                                                                                                                                                                                                                                                                                              gastritis and inflammation.
                                                                                                                                                                                                                                                               Sequence
                              121 VYDQSYFPSTIVTKWDLYCDYQSLKSVVQFLLLTGMLYGGIIGGHVSDR------- 169
                                                           61 asilgsispeallaisippgpnqrphqcrrfrqpqwqlldpnatatswseadtepcvdgw 120
                                                                                                                                                       1 MAFBELLSOYGGLGREOMLHLYFILESLMLLIPHILLENFAAAIPGHRCWYHMLDNNTGS 60
                                                                                                                         1 mafselldlvgglgrfqvlqtmalmvsimwlctqsmlenfsaavpshrcvaplldnstaq 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Lal P,
A, Walia NK, Gar
On M, Greene BD,
                                                                                            GNETGILSEDALLRISIPLDSNLRPEKCRREVHPOWOLLHLNGTIHSTSEADTEPCVDGW 120
   vydrsiftstivakwnivcdshalkpmaqsiylagilvgaaacgpasdrfgrrlvltwsy 180
                                                                                                                                                                                           Similarity 37.8
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0193500.
                                                                                                                                                                                                                                                                      553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Sugar_transporter 204..222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Sugar_transport_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Sugar_transport_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lal P, Policky JL, Nguyen DB, i
K, Gandhi AR, Tribouley CM, Pati
ne BD, Hernandez R, Borowsky ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383
                                                                                                                                                                                                         42.7%; Score 601; DB 22; Length 553; 37.8%; Pred. No. 5.3e-56;
                                                                                                                                                                                                30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           patterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Au-Young J, atterson C;
                                                                                                                                                                                                         Indels 108; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 dystrophy) or
169
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, consumpressant and cytostatic activity. The polynucleotides are useful consumpressant and cytostatic activity. The polynucleotide or polynucleotide consumpressant and cytostatic activity. The polypeptide or polynucleotide consumpressant and composition containing a polypeptide or polynucleotide consistency of the peripheral nervous system diseases, such as consistency and central nervous system diseases, such as consumpressant activity and central nervous system diseases, anyotrophic constant sclerosis, and shy-Drager Syndrome. Other uses include the constant of the activities such as: Immune system suppression, activity, chamotactic/chemokinetic activity, haemostatic conditions activity, chamotactic/chemokinetic activity, haemostatic conditions activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and constants and constants are proposed to the constants and constants are proposed to the constants and constants and inflammation, leukaemias and constants are proposed to the constants and constants and constants.
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25-APR-2000; 2000US-0552317.

29-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

19-JUL-2000; 2000US-0653450.

03-AUG-2000; 2000US-0653191.

14-SSP-2000; 2000US-0631936.

19-CCT-2000; 2000US-06319344.

29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 lqmavmgtaaafapafpvyclfrfllafavagvmmntgtllmewtaararplvmtlnslg 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM41845 standard; Protein; 369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || ||||||: | :|| ||: |
241 fsfghgltaavaygvrdwtllqlvvsvpfflcflyswwlaesarwllttgrldwglqelw 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 -----WLVESARWLIITNKLDEGLKALR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; peripheral nervous system; neuropathy; central nervous system; classe; Huntington's disease; haemostatic; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; thrombolytic; drug screening; arthritis; inflammation; chemokinetic; thrombolytic; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polypeptide SEQ ID NO 6776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM41845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 rvaaingkgavqdtitpevllsamreeismgqppaslgtllrmpglrfrtci 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 KVARTINGIKNAEETLNIEVVRSTMOEELDAAQTKTTVCDLFRNPSMRKRICI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \dot{\ }
                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAI61001
                                                                                                                                                                                                                                                                                                     Example 2; SEQ ID NO 6776; 10078pp; English.
      C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                              2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang D;
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specification Note:

The sequence data for this patent did not form part of the printed

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RESULT 11
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Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                  N-PSDB; AAD12607
                                                                                                         Kato S, Kimura T;
                                                                                                                                                                                06-JAN-2000; 2000JP-0000585.
06-JAN-2000; 2000JP-0000588.
11-JAN-2000; 2000JP-0002299.
03-FEB-2000; 2000JP-0026662.
                                                                                                                                              (PROT-) PROTEGENE INC
                                                                                                                                                                           03-MAR-2000;
                                                                                                                                                                                                                                                  28-DEC-2000; 2000WO-JP09359.
                                                                                                                                                                                                                                                                                                                                                     Human; hydrophobic domain; gene therapy; nutritional supplement; cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritts; insulin-dependent diabetes; haematopolegis; tissue growth activity; Parkinson's disease; oytostatic; huntington's disease; Albeimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
                                                                                                                                                                                                                                                                                                             WO200149728-A2.
                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein having hydrophobic domain, HP03882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE06612 standard; Protein; 550 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 rsgmknardtitleilkstmkkeleaaqkkkpflgerlhmpnickrisllpftk 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 TNGIKNAEETLNIEVVRSTMQEELDAAQTKTT-VCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 fmtlaglafairdwhilqlvvsvpyfvifltsswilesarwliinnkpeeglkeirkaah 248
                                                                              2001-418355/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 ivgtcaalaptfliycslrflsgiaamslitntimliaewathrfqamgitlgmcpsgia 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 SYFPSTIVTKWDLVCDYQSLKSVVQELLLTGMLVGGIIGGHVSDR------- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 isfsstivtewdivcdsqsitsvakfvfmagmmvggilgghlsdrfgrrfvlrwcylqva 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 GILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGWVYDQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 galsqdailrisipldsnmrpekcrrfvhpqwqllhlngtfpntsdadmepcvdgwvydr 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                  SAGAMI CHEM
                                                                                                                                                                     2000JP-0058367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 AA;
                                                                                                                                                                                                                                                                                                                                                  antiinfertility; antiinflammatory.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----WLVESARWLIITNKLDEGLKALRKVAR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.3%; Score 594.5; DB 22; Length 369;
41.8%; Pred. No. 1.5e-55;
tive 30; Mismatches 32; Indels 109;
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AAB69091
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                 Human; organic anion transporter; OAT4; nephrotrophic; kidney disease; abnormal foetal growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                  Human organic anion transporter OAT4 protein sequence SEQ ID NO:2.
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                                                                                                                                                          24-APR-2001 (first entry)
                                                                                                                                                                                                                                               AAB69091 standard; Protein; 550 AA
                                                                                                                                                                                                                    AAB69091;
                                                                                                                                                                                                                                                                                                                                    296 lrkvaringhkea-knitievimssvkeevasakeprsvidifcvpvirwrscami 350
                                                                                                                                                                                                                                                                                                                                                                                 191 LRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILV 246
                                                                                                                                                                                                                                                                                                                                                                                                                              236 cafsagqaalgglafalrdwrtlqlaasvpffaisliswwlpesarwliikgkpdqaiqe 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 -----WLVESARWLIITNKLDEGLKA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 cclqlavagtstifaptfviycglrfvaafgmagiflssltlmvewtttsrravtmtvvg 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 GWVYDQSYEPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR----- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 gwvydrsvftstivakwdlvcssqglkplsqsifmsgilvgsfiwgllsyrfgrkpmlsw 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 GSGNETGILSEDALLRISIPLDSNLRÞEKCRRFVHÞOWQLLHLNGTIHSTSEADTEÞCVD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 gsavstn-mtpkalltisippgpnggphgcrrfrgpgwglldpnatatswseadtepcvd 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 mafskllegaggvglfqtlqvltfilpclm--ipsqmllenfsaaipghrcwthmldn-- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAFEELLSQVGGIGREQMLH-LVFILPSLMLLIP-HILLENFAAAIPGHRCWVHMLDNNT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 42.1%; Score 592; DB 2 Local Similarity 40.2%; Pred. No. 5e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _ DB_22; Length 550;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human placental organic anion transporter, designated OAT4. OAT4 has nephrotrophic activity. The OAT4 transporter, designated OAT4. OAT4 has nephrotrophic activity. The OAT4 protein and encoded gene are useful in studying causes of abnormality, including the application of a variant nucleic acid as a probe to detect the presence of a gene encoding the transporter OAT4, or to identify or the presence of a gene encoding the transporter OAT4, or to identify or quantify such gene, and in developing drugs to prevent or treat various quantify such gene, and in developing drugs to prevent or treat various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            placental organic anion transporter gene and encoded polypeptide OAT4, useful in studying causes of abnormality, and in developing drugs to prevent or treat various kidney diseases and abnormal fetal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 26-28; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kidney diseases and abnormal foetal growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           119
                                                                                                                                       AAE10336 standard; Protein; 566 AA
                                                                                                                                                                                                                                                                                                                                 176 cclqlavagtstifaptfviycglrfvaafgmagiflssltlmvewtttsrravtmtvvg 235
Human; transporter and ion channel; TRICH-13; therapy; akinesia; neurological disorder; immune disorder; allergy; nootropic; dementia;
                                                                                                                                                                                                                                           191 LRKVARTNGIKNAEETLNIEVVRSTMGEELDAAGTKTTVCDLFRNPSMRKRICILV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
                                          Human transporter and ion channel-13 (TRICH-13) protein
                                                                                                           AAE10336;
                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAFEEULSOVGGLGREOMLH-LVFILPSLMILIP-HILLENFAAAIPGHRCWVHMLDNNT 58
                                                                               10-DEC-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gwvydrsvftstivakwdlvcssqglkplsqsifmsgilvgsfiwgllsyrfgrkpmlsw 175
                                                                                                                                                                                                                                                                                                                                                                                                                         GWYYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                    gsavstn-mtpkalltisippgpnggphgcrrfrgpgwglldpnatatswseadtepcvd 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSGNETGILSEDALLRISIPLDSNLRPEKCRREVHPQWQLLHLNGTIHSTSEADTEPCVD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143; Conservative
                                                                                                                                                                                                                                                                         cafsagqaalgglafalrdwrtlqlaasvpffaisliswwlpesarwliikgkpdqalqe 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF32614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 42.18;
Similarity 40.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        550 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score 592; DB 2
pred. No. 5e-55;
                                                                                                                                                                                                                                                                                                                ....-------WLVESARWLIITNKLDEGLKA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                         _____ 169
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                             QY
                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2000; 2000US-0184866.
02-MAR-2000; 2000US-0187947.
09-MAR-2000; 2000US-0188333.
17-MAR-2000; 2000US-0190230.
17-MAR-2000; 2000US-0190277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastritis; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-FEB-2001; 2001WO-US05942
                                                                                                                                                                                                                                                                                                                The present sequence is human transporters and ion channels (TRICH-13) protein. The TRICH DNA, protein and their agonist and transporters are useful in the diagnosis, treatment and prevention of antagonists are useful in the diagnosis, treatment and prevention of transport disorders (akinesia, amyotrophic lateral sclerosis, cystic transport disorders (akinesia, amyotrophic lateral sclerosis, cystic transport disorders (e.g. cardiomyopathy, Becker's muscular dystrophy) or immunological disorders (e.g. allergies, acquired immunodeficiency syndrome (AIDS), Crohn's disease, rheumatoid arthritis, scleroderma, syndrome (AIDS), viral, bacterial, parasitic, protozoal and multiple sclerosis, viral, bacterial, parasitic, protozoal and helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis, helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thirteen human transporters and ion channels (referred to as TRICH-1 to TRICH-13), useful in the diagnosis, treatment and prevention of transport (e.g. akinesia), neurological, muscle or immunological disorders (e.g. allergies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 119-120; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thornton M,
                                                                                                                                                                                                                                                                                                      gastritis and inflammation.
                                                                                                                                                                                                                                                                        Sequence
119 GWYYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------ 169
                                                                                                                                                                                                            Local
                                                                                                59
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                                                                  57
                                                                                                                                                           1 MAFEELLSQVGGLGREQMLH-LVFILPSLMLLIP-HILLENFAAAIPGHRCWVHMLDNNT 58
                                                                                                                            1 mafskllegaggyglfgtlgvltfilpclm--ipsgmllenfsaalpghrcwthmldn-- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-582050/65.
                                                                                            GSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWOLLHLNGTIHSTSEADTEPCVD 118
                                                             gsavstn-mtpkalltisippgpnggphqcrrfrgpqwqildpnatatswseadtepcvd 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rang YT, L
, Walia NK,
                                                                                                                                                                                                140;
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                                                                                                                                                                                                                Similarity
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2000US-0188333.
2000US-0190230.
2000US-0192077.
2000US-0193500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Greene BD,
                                                                                                                                                                                                                                                                               566 AA;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /laber=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation.
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BD, Hernandez R,
                                                                                                                                                                                                                  42.0%; Score 590.5; DB 2
39.0%; Pred. No. 7.6e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Policky JL,
                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y JL, Nguyen DB,
Tribouley CM, P
                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borowsky ML,
                                                                                                                                                                                                                                          DB 22; Length 566;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Au-Young J, atterson C;
                                                                                                                                                                                                                Indels 115;
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The present sequence is human protein with hydrophobic domain, Hp03613.
The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with the interpretate polypeptide expression. The polynucleotides may be used cell and culturing the cell to express the protein. The polynucleotides can be used its complementary sequences may also be used as DNA probes in the golynucleotides may sequences may also be used as DNA probes in the production of antibodies and in assays and also used in gene therapy. The polypeptides may complementary sequences may also be used as DNA probes in the production of antibodies and in assays and also used in gene therapy. The polypeptides may complements of polypeptide expression and activity. The complements, in the production of antibodies and in assays to modulate cytokine and cell proliferation activity, to modulate complements, immune stimulation or suppression (e.g. for the treatment of microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                       Claim 1; Page 59-60; 563pp; English.
                                                                                                                                                                                                                                                                                                              Alzheimer's and inflammation
                                                                                                                                                                                                                                                                                                        Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD12566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JAN-2000; 2000JP-0000585.
06-JAN-2000; 2000JP-0000588.
11-JAN-2000; 2000JP-0002299.
03-FEB-2000; 2000JP-0026862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PROT-) PROTEGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-DEC-2000; 2000WO-JP09359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200149728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contraceptive; antiinfertility; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; hydrophobic domain; gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein having hydrophobic domain, HP03613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE06571 standard; Protein; 578 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 LRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 irkvaringhkeetecvylkvlmssvkeevasakeprsvldlfcvpvlrvrscamlvvk 354
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RESULT 15
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        Tang YT,
                                      (HYSE-) HYSEQ INC.
                                                                      18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                                                                                                          16-APR-2001; 2001WO-US08656.
                                                                                              18-APR-2000;
                                                                                                                                                                      25-OCT-2001.
                                                                                                                                                                                                          WO200179449-A2.
                                                                                                                                                                                                                                                    Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi
                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                            Novel human secreted protein #2870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU32379 standard; Protein; 645 AA.
                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 slgtllrmpglrfrtci 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 TVCDLFRNPSMRKRICI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 swwlaesarwllttgrldwglqelwrvaaingkgavqdtltpevllsamreelsmgqppa 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 --WLVESARWLIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMOEELDAAOTKT 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate haematopoiesis, to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 asilgslspeallaisippgpnqrphqcrrfrqpqwqlldpnatatswseadtepcvdgw 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vydrsiftstivakwnlvcdshalkpmaqsiylagilvgaaacgpasdrfgrrlvltwsy 180
  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    578 AA;
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Drmanac RT
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35.3%; Pred. No. 1.3e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 578;
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NX Nucleic acids encoding a range of human polypeptides, useful in genetic production, testing and therapy.

Nucleic acids encoding a range of human polypeptides, useful in genetic production, testing and therapy.

XX Claim 20; Page 597; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The CC polypeptides and antibodies to the polypeptides are useful for control of the polypeptides are useful for identifying agents (agonists and antagonists) that bind to them. Cells capressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising compineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in treatment of leukaemias. Anu29510-Anu33304 represent the amino acid sequences of novel human secreted proteins of the invention.

Output Match 133.6%; Score 472; DB 22; Length 645;

рь Qy В δĀ Qy В δÃ 밁 Qy 밁 Š Š 밁 Ş В Query Match Best Local S Best Local Similarity Matches 126; Conserv 170 116 lkplsqsifmsgilvgsfiwgllsyrfgrkpmlswcclqlavagtstifaptfviycglr 175 236 aasvpffaisliswwlpesarwliikgkpdgalgelrkvaringhkeaknltietppppp 295 170 176 fvaafgmagiflssltlmvewtttsrravtmtvvgcafsagqaalgglafalrdwrtlql 235 144 LKSVVQFLLLTGMLVGGIIGGHVSDR----- 169 232 LFRNPSMRKRICILVFLR 249 356 insthtvtsithhlhhvarthlmgvldvsgetecvylkvlmssvkeevasakeprsvld 415 296 pipipsptapplstptitftaitpsppappipsltpqppslqnisttfttivtignstii 355 56 gphqcrrfrqpqwqlldpnatatswseadtepcvdgwvydrsvftstivakwdlvcssqg 115 84 RPEKCRREVHPQWQLLHLNGTIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQS 143 25 LPSLMLLIP-HILLENFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISIPLDSNL 83 1 lpclm--ipsqmllenfsaaipghrcwthmldn--gsavstn-mtpkalltisippgpng 55 ------WLVESARWLITNKLDEGLKALRKVARTNGTKNAE----lfcvpvlrwrscamlvvk 433 Conservative :: = 33.6%; Score 472; DB 22; Length 645; 28.8%; Pred. No. 6.3e-42; ative 31; Mismatches 63; Indels 218; Gaps --ETLNIEVVRSTMQEELDAAQTKTTVCD 231 204 204 6

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     protein search, using sw model
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4: /ggn2_6/ptodata/2
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US-08-964-127-2
US-08-964-127-4
US-09-96-692-2
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US-09-96-692-7
US-09-98-386-7
US-09-98-386-7
US-09-187-050-12
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Query Match 12.1%; Score 169.5; DB 3; Length 556; Best Local Similarity 20.5%; Pred. No. 7.8e-11; Matches 77; Conservative 47; Mismatches 95; Indels 157; Gaps 15;	Que Bes Mat
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DEDNESS:	٠. ٠.
TYPE: amino acids	٠. ٠.
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TRATION NUMBER: 35,391	٠. ٠.
증진	•• ••
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APPLICATION NUMBER: US/08/501,572	• •• •
SOFTWARE: PatentIn Release #1.0, Version #1.30	
ER: IBM PC compatible	٠. ٠.
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	٠. ٠.
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STREET: 1300 I Street, N.W., Suite 700	• • •
DENCE ADDRESS	•• ••
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OF INVENTION: Transport protein Which Effects The OF INVENTION: Transport Of Cationic Year Proteins	٠. ٠.
CANT: Grundeman, Dirk CANT: Gorboulev, Valentin	
ANT: Koepsell, H	
Patent N. 10036323	 . G
1 Application	RES
268 KFSRALKTLQRVATENGKKEEGEKLTVEELKFNLQKDITSAKVKYGLSDLFRVSILRR	Ъ
183 KLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMOEELDAAOTKTTVCDLFRNDSMBK 24	٠ Ω٧
208 AISSTTIGYCYTIGQFILPGLAYAVPQWRWLQLSVSAAFFIFSLLSWWVPESIRWLVLSG	Ф
170WIVESARWLIITN	Qy
148 GRKPILTWSYLLLAASGSSAAFSPSLTVYMIFRFLCGCSISGISLSTIILNVEWVP	Db
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111 ADTEPCYDGWYYDOSYFPSTIYTKWDIYOTONGIX SINYOFII TOOYI YOOTTO	δõ
61 V	Дb

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; MOLECULE TYPE: peptide US-09-040-444-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 556 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Koepsell, Hermann
APPLICANT: Koepsell, Hermann
APPLICANT: Grundeman, Dirk
APPLICANT: Koepsell, Hermann
APPLICANT: Grundeman, Dirk
APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
/ Match 12.1%; Score 169.5; DB 3; Length 556; Local Similarity 20.5%; Pred. No. 7.8e-11; nees 77; Conservative 47; Mismatches 95; Indels 157
                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: O'Connor, Steven P
REGISTRATION NUMBER: 41,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/0 FILING DATE: March 18, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P. 1300 I Street, N.W., Suite 700
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Matches

Indels 157; Gaps

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RESULT A OB-501-572-3 INS-OB-501-572-3 PATENT NO. 6053673 PATENT OF INVENTION: Transport of Cattonic Xenoblotics and/or Pharmaceuticals, Patent No. 6053673 PATENT OF INVENTION: Transport of Cattonic Xenoblotics and/or Pharmaceuticals, Patent Of Invention, Patent No. 605000000 PATENT OF INVENTION: DAY SEQUENCES: 6 NUMBER OF SEQUENCES: 6 NUMBER OF SEQUENCES: 6 NUMBER OF SEQUENCES: 6 NUMBER OF SEQUENCES: 6 COMPTER OF SEQUENCES: 6 COMPTER TO COMPTER OF SEQUENCES: 6 OPERATOR USA ZIT: 2000-3115 COMPTER READABLE FORM: N.W., Suite 700 OPERATOR SYSTEM PC. COMPATION: OPERATOR OF SEQUENCES OF PATENTION UNDERS: 100 1 Street, N.W., Suite 700 OPERATOR SYSTEM PC. COMPATION: APPLICATION NUMBER: US.008/ONS-DOS OPERATOR OF SEQUENCE OF STANDERS: 35.391 REGISTRATION UNDERS: US.008/501.572 PATENTION UNDERS: US.008/501.572 REFERENCE/JOIN UNDERS: 35.391 REGISTRATION UNDERS: 35.391 REGISTRATION NUMBER: 02.441.1453-00000 TELEPONDATION UNDERS: 35.391 REFERENCE/JOIN UNDERS: 35.391 REGISTRATION UNDERS: 35.391 REG	
RESULT Sequence 562766 Sequence 562766 Patent 0 INFORMATION: Chemistry Che	Query Match Best Local Similarity 10.8%; Pred. NO. 7.1e-09; Indels 139; Gaps 12; Best Local Similarity 10.8%; Pred. No. 7.1e-09; Indels 139; Gaps 12; Best Local Similarity 10.8%; Pred. No. 7.1e-09; Indels 10.9%; Indels 139; Gaps 12; Best Local Similarity 10.8%; Pred. No. 7.1e-09; Indels 12.1e-09; Indels 139; Gaps 12; Best Local Similarity 10.8%; Pred. No. 7.1e-09; Indels 12.1e-09; Indels 139; Gaps 12; Best Local Similarity 10.8%; Pred. No. 7.1e-09; Indels 139; Gaps 12; Best Local Similarity 10.8%; Pred. No. 7.1e-09; Indels 139; Gaps 12.2e-09; Indels 139; Gaps 12.2e-09; Indels 139; Indels

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US-09-040-444-3
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INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS.
LENGTH: 553 amino acids
                                                                                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Toohey, Kimberlin M
REGISTRATION NUMBER: 35,391
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100044000
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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TITLE OF INVENTION: Transport protein which Effects The
TITLE OF INVENTION: Transport Of Cationic Xenobiotics and North Pharmaceuticals,

NA Sequences Encoding It And Their Use.
                                 TYPE:
              STRANDEDNESS:
      TOPOLOGY:
                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 RIIKHIAKKNG-----KSLPASLORLRLEEE-TGKKLNPSFLDLVRTPQIRKHTMILMY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 KALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVF 247
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                         amino acid
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linear
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1300 I Street, N.W., Suite 700
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                                    amino acids
            single
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TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO:
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            ATTORIEX/AGENT INFORMATION:
NAME: O'CONDOX, Steven P
REGISTRATION NUMBER: 41,225
REFERENCE/DOCKET NUMBER: 2481.1453-01
TELEPHONE: (202)408-4000
TELEPHONE: (202)408-4000
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                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                              CLASSIFICATION
                                                                                                                       APPLICATION NUMBER: FILING DATE: March
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    2, Application US/09040444
5. 6063766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocal Similarity
S 75; Conserv
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Gorboulev, Valentin
WENTION: Transport protein Which Effects The
WENTION: Transport Of Cationic Xenobiotics and or Pharmaceuticals,
The Sequences Encoding It And Their Use.
                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                            Koepsell, Hermann
                                                                                                                       March 18, 1998
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                                                                                                                                US/09/040,444
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20.4%; Pred. No. 3.9e-08;
ative 34; Mismatches 117; Indels 142; Gaps
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14;

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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-040-444-2
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US-08-964-127-2
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Best Local Similarity
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Patent No. 6277565
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Grandearl, Andrew David John
TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                    APPLICATION NUMBER: US/08/964,127
FILING DATE: 06-NOV-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 QKRNTEAIKIMDHIAQKNG-KLPPADLKMLSLEEDVTEKL----SPSFADLFRTPRLRK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 SRRTVAIMYQMAFTVGLVALTGLAYALPHWRWLQLAVSLPTFLFLLYYWCVPESPRWLLS 291
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                                                  ATTORNEY/AGENT INFORMATION: NAME: Crews, Ph.D., L. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 RTFILMYL 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 -----WSPAEELNYTVP----GLGPAGEAFLGQCRRY-EVDWNQSALSCVDPLASLATNR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GNETGILSEDALLRISIPLDSNLRPE-----KCRRFVHPQWQLLHLN-----GTIHST 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 EELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRC----WVHMLDNNTGS 60
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
TOWNEL CROWS, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,567
REGISTRATION NUMBER: 07334/038001
                                                                                                                                                                                                                                                                                                                                           ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                            FILING DATE:
                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                  USA
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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-964-127-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/09496692
; Patent No. 6313271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Grandearl, Andrew David John
TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: UTELEFAX: 200154
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
OPERATE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                     APPLICATION NUMBER: 08/964,127
FILING DATE: 06-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 TYCDL-----FRNPSMRKRICILVFLRKKISRKRHKNDCYTKV 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 PGLFLESARWLIVKRQIEEAQSVLRILAERN--RPHGQMLG-----EEAQEALQDLE 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 NTCPLPATSSFSFASLLNYRN--IWKNLLILGETNFIAHAIRH---CYQPV 328
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TELEPHONE: 01/,542-8906
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                                                                                                                                                                                                                                                                                                  ZIP:
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish ...
STREET: 225 Franklin Street
                                                                                                                            APPLICATION NUMBER: FILING DATE:
NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,567
                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGYLFLGYPADRFGRRGIVLLTLGLVGPCGVGGAAAGSSTGVMALRFLLGFLLAGVDLGV 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 7.4%; Score 104; DB 4; Length 520; Similarity 18.2%; Pred. No. 0.0025; 64; Conservative 33; Mismatches 92; Indels 162;
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US-08-928-692-12
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
CADDRESSEE: No. 59587270 No. 5958727d1sk of No. 5958727th America, Inc.
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TITLE OF INVENTION: Met
TITLE OF INVENTION: a P
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
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                                         CLASSIFICATION:
                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Wil
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                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10174
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 NFAAAIPGHRCWYHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRRFYHPQWQL 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yaver, Deborah S.
Lamsa, Michael
                                                                                                                                                                                           FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methods for Modifying the Production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----EEAQEALQDLE 282
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US-08-964-127-4
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                                                                        INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,127
FILING DATE: 06-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                          REFERENCE/DOCKET NUMBER: 07334/038001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,5
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Grandearl, Andrew David John
TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
TITLE OF INVENTION: MOLECULES
                                                                            TELLEFAX: 01.
TELEFAX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                    LENGTH:
TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 LDEEVKAKQSLKRLRGYDDVTKDIN-----EMRKEREEASSEQKVSIIQLFTNSSYRQP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 LDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAA--QTKTTVCDLFRNPSMRKR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 QLAIVTGILISQIIGLEFILGNY-DLWHILLGLSGVRAILQSLLLFFCPESPRYLYI--K 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 QFLLLTGMLVGGIIG-----GHVSDRWLV------ESARWLIITNK 183
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 ILVALML 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                : 286 amino acids amino acid
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                                                                                                        617/542-8906
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27.6%; Pred. No. 0.0072;
ative 22; Mismatches 3
                                                                                                                                                                                  P-43,567
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US-08-964-127-4
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FRAGMENT TYPE:
                                                        TELEX: 200154
[NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Grandearl, Andrew David John TITLE OF INVENTION: NOVEL GENES ENCODING TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 ------ 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 -----LTGMLVGGI---- 161
                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070 TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 PGLFLESARWLIVKROIEEAQSVLRILAERNRPHGQMLGEEA------QEALQDLE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 ---LVESARWLIITNKLDEGLKALRKVA---RTNGIKNAEETLNIEVVRSTMQEELDAAQ 224
                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 SST 285
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                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 HYGAFPPNASGW-EQPPNASGVSVASAALAASAASRVATSTDPS-----CSGFAPP---- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 NFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 -----DFNHCLKDWDYNGLPVLTTNAIGQWDLVCDLGWQVILEQILFILGFA 112
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                                                                                                                                                       NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,567
REFERENCE/DOCKET NUMBER: 07334/038001
                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 06-NOV
                                                                                                                                                                                                                                                                                             FILING DATE:
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                LENGTH:
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amino acid
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17.8%; Pred. No. 0.0043;
ative 29; Mismatches 73; Indels 147; Gaps
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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-09-496-692-4
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US-08-989-386-7
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Sequence 7, App. 100
Sequence 7, App. 100
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Sequence 7, App. 100
Sequence 8, App. 100
Sequence 10
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MEDIUM TYPE: Diskett
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                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 YLMRLELCDPTORLRVALAGELVGVGGHFLFLGLALVSKDWRFLQRMTTAPCILFLFYGW 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 SGYLFLGYPADRFGRRGIVLLTLGLVGPCGVGGAAAGSSTGVMALRFLLGFLLAGVDLGV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 -----LTGMLVGGI---- 161
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 NFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 SST 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 LHLNGTIHSTSEADTEPCVDGWVYD-QSYFPSTIVTKWDLVCD--YQSLKSVVQFLL--- 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/989,386
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Guegler, Karl J.
Corley, Neil C.
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; LIBRARY: GenBai
; CLONE: 894162
US-08-989-386-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09031392 Patent No. 5942398
                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               welly match 6.2%; Score 87; DB 2; Length 581; Best Local Similarity 25.1%; Pred. No. 0.26; Matches 53; Conservative 24. William 1.20
 MOLECULE TYPE:
                                                                                                                                                                                            APPLICATION NUMBER: US/09/031,392
FILING DATE: 26-FEB 1998
ATTORNEY_AGENT INFORMATION:
NAME: Me1klejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
TIC //04 //21 242
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                            TELEFAX: UI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
NUMBER OF SEQUENCES: 10
             LENGTH: 49# ...
TYPE: amino acid
Tinear
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LENGTH: 581 amino acids
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                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
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; Sequence 5, Application US/09299549

; Patent No. 6136547
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                                                                                                                                                                          Matches
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                                                                                                                                                                                        Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acid
TYPE: amino acid
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Best Local 9
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NAME: Meiklejohn, Ph.D., Anita L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/031,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: DATA: 05/09/299,549
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MEDIUM TYPE: Diskett
229 LWGTEDVAQDIQEMKDESMRMSQEKQV-----TVLELFRAPNYRQPIIISIMLQ 277
                                    194 VARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFLR 249
                                                                            184 WPLLLGFTILPATIQCAALP-------FCPESPRFLLINRKEEEKAKEILQR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: GLUTEX AND USES THEREOF
                                                                                                                  135 WDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRWLVESARWLIITNKLDEGLK-ALRK 193
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ADDRESSEE: Fish & Richardson P.C.
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TELEFAX: 617/542-8906
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CITY: Boston
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il Similarity 23.3%; Pred. No. 0.52;
27; Conservative 26; Mismatches
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23.3%; Pred. No. 0.52;
ative 26; Mismatches 40; Indels 2;
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Search completed: July 1, 2002, 11:39:26 Job time: 172 sec

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Maximum Match 100%
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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195.5
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GTR2_MOUSE
C11A_MOUSE
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GTR3_CHICK
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GTR1_HUMAN
GTR3_RABIT
YD56_YEAST
                                                                                                                                                                                                                                                                                                                                                                     GTR3_SHEEP
C11A_CAPHI
GTR1_CHICK
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GTR1_MOUSE
GTR1_RABIT
GTR1_RAT
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                    C11A_HORSE
SDC4_HUMAN
YM31_MYCTU
C11A_BOVIN
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Q61576 mus musculu
P28568 gallus gall
P7793 thermotoga
p58352 bos taurus
p47843 ovis aries
P47843 ovis aries
P479153 capra hircu
p46896 gallus gall
Q92339 schizosacch
P11166 homo sapien
Q9xsc2 oryctolagus
Q04399 saccharomyc
P10612 sus scrofa
p53166 saccharomyc
Q50676 mycobacteri
P05108 homo sapien
p49071 drosophila
p13355 oryctolagus
p13155 oryctolagus
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070594 rattus norv
076082 homo sapien
P11168 homo sapien
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Q9qz82
P12336
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      Q9ept4
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O46515
P31431
Q10503
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                                                                                                     caenorhabdi
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IG-OCT-2001 (Rel. 40, Last Ocganic cation/carnitine to member 5) (High-affinity successed of Cornal Carnitine to member 5) (High-affinity successed of Cornal Mus musculus (Mouse). Eukaryota; Metazoa; Chorda Musmanalia; Eutheria; Rodeni NCBI_TAXID-10090; [1] SEQUENCE FROM N.A. STRAIN-C57BL/6J; TISSUE=K MEDLINE=99113835; PubMed=Wishino M., Kato H., Oku A. Nikaido H., Sai Y., Koizu Yashino M., Kato H., Oku A. Nikaido H., Sai Y., Koizu Yashino M., Kato H., Ohur Tsuji A.; "Primary systemic carniti gene encoding sodium ion-wat. Genet. 21:91-94(1999) [2] EQUENCE FROM N.A., AND V STRAIN-C3H; MEDLINE=99057546; PubMed=Lu K., Nishimori H., Naka Namissense mutation of manissense mut	1 ISE I2_MOUSE IOE8; OCT-2001	78.5 77.5 77.7 77.7 77.7 77.7 76.5 76.5 76
-2001 (Rel. 40 -2001) (Rel. 40 -2010) (Rel. 40 5) (High-affi) 5) (Righ-affi) 5) OR OCTN2. 5 OR OCTN2. 5 CULUS (MOUSE) 0ta; Metazoa; ia; Eutheria; axID-10090; CCE FROM N.ACS7BL/6J; TIS E-99113835; PR E-9913835; PR E-9913835; PR E-9913835; PR INCE FROM N.A., A-C3H; A	ST. (Rel.	
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craniata; Vertebrata; Sciurognathi; Muridae; Sciurognathi Sciuro	ALIGNMENTS PRT; 557 AA. sequence update)	GTR3_CANFA AGTR3_MOUSE PHY_MOUSC VSP1_ARATH C11A_RAT SPPA_HAEIN RIP2_MOUSE YPT1_PHYIN GTR3_HUMAN APX_XENLA VN34_ROTS4 Y433_MYCTU
ine cotransporter). La: Euteleostomi; dae: Murinae: Mus. G., Matsuishi T., akawa J., Shimane M., by mutations in a nsporter."; jima M.; pendent carnitine ess mouse."; carnitine ry CARNITINE s WITHOUT THE ve CELLULAR UPTAKE OF tein. F JUVENILE VISCERAL F JUVENILE VISCERAL F JUVENILE VISCERAL F GAMILY. ORGANIC ced through a collaboration and the EMBL outstation re no restrictions on its ts content is in no way		p47842 canis famil p98200 mus musculu p33529 mougeotia s 049195 arabidopsis p14137 rattus norv p45243 haemophilus p97433 mus musculu Q01890 homo sapien Q01613 xenopus lae Q00721 simian 11 r p96279 mycobacteri

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RESULT
OCN2_RAT
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                        OCN2_RAT STANDARD; PRT; 557 AA.

070594; 090WLO;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Organic cation/carnitine transporter 2 (Solute carrier family 22,
Organic cation/carnitine codium-docardant carnitine contangency 22,
                member 5) (High-affinity sodium-dependent carnitine cotransporter)
                                                                                                                                                                                      327 QLHHIYDLIRTRNIRVITIMSIILWLTIS 355
                                                                                                                                                                                                                   228 T---VCDLFRNPSMRKRICILVFLRKKIS 253
                                                                                                                                                                                                                                                                          172 V-ESARWLIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTM----QEELDAAQTKT 227
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                                                                                                                                                                                                                                                                                                                                                                                                                            97 LEPGRDVDLEQLEQESCLDGWEYDKDVFLSTIVTEWDLVCKDDWKAPLTTSLFFVGVLMG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 LSSAWRNH------SIPLETKDGRQVPQKCRRY-----RLATIANFSELG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDEVTAFLGEWGDFQ--RLIFFLLSAS-IIPNGFNGMSIV---FLAGTPEHRCLVPHTVN 57
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TE; PS00216; SUGAR_TRANSPORT_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Pharmacol. Exp. Ther. 290:1482-1492(1999).

-I- FUNCTION: SODIUM-ION DEPENDENT, HIGH AFFINITY CARNITINE
TRANSPORTER. ALSO TRANSPORTS ORGANIC CATIONS WITHOUT THE
INVOLVEMENT OF SODIUM. INVOLVED IN THE ACTIVE CELLULAR UPTAKE
                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITINE-99384224; pubMed-10454528; Wu X., Huang W., Prasad P.D., Seth P., Rajan D.P., Leibach F.H., Chen J., Conway S.J., Ganapathy V., "Functional characteristics and tissue distribution pattern of organic cation transporter 2 (OCTN2), an organic cation/carnitine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 251:586-591(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning and characterization of high-affinity carnitine transporter from rat intestine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=SPRAGUE-DAWLEY; TISSUE-Intestine; MEDLINE=99011422; PubMed=9792817;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kanai Y., Endou H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEBS Lett. 425:79-86(1998).
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SLC22A5 OR OCTN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. ORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN THE PROXIMAL AND DISTAL TUBULES
AND IN THE GLOMERULI IN THE KIDNEY, IN THE MYOCARDIUM, VALVES, AND
ARTERIOLES IN THE HEART, IN THE LABYRINTHINE LAYER OF THE
PLACENTA, AND IN THE CORTEX, HIPPOCAMPUS, AND CEREBELLUM IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                  CATION SUBFAMILY.
                                                                                                                                                                                                          PS00216;
                                                                                                                                                                                                                                  IPR003662; sub_transporter
                                                                                                                                                                                      Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _ Kusuhara H., Utsunomiya-Tate N., Tsuda M., Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spitzenberger F., Engelhardt M., Martel F., Oerding
                                                                                                                                                                                                     SUGAR_TRANSPORT_1;
                                                                                                                                                                                     Glycoprotein
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SEQUENCE
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CARBOHYD
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O76082;
                                                                                                                                                                                                MEDITINE-98289574; PubMed-9618255; Wu X., Prasad P.D., Leibach F.H., Ganapathy V.; CDNA sequence, transport function, and genomic organization of human OCTN2, a new member of the organic cation transporter family."; Blochem. Biophys. Res. Commun. 246:589-595(1998).
                                                                                                                                                                                                                                                                                                                                                                                                        Organic cation/carnitine transporter 2 (Solute carrier family 22)
                                                                                                                                                                                                                                                                                                                                                                          member 5) (High-affinity sodium-dependent carnitine cotransporter). SLC22A5 OR OCTN2.
                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                           "Molecular and functional identification of sodium ion-dependent, high affinity human carnitine transporter OCTN2.";
J. Biol. Chem. 273:20378-20382(1998).
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                          TISSUE=K1dney;
MEDLINE=98352077; PubMed=9685390;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                      Tamai I., Ohashi R., Nezu J.-I., Yabuuchi H., Oku A., Shimane
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
   MEDLINE-99113835; PubMed-9916797;
Nezu J., Tamai I., Oku A., Ohashi R.,
                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 RTRNIR 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFGRKNVLFLTMGMQTGFSFLQLFSVNFEMFTVLFVLVGMGQISNYVAAFVLGTEILSKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDEVTAFLGEWGPFQ--RLIFFLLSAS-IIPNGFNGMSIV---FLAGTPEHRCLVPHTVN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQGRVKEAEVIIRKAAKFNGI------VAPSTIFDPSELQDLNSKKPQSHHIYDLV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTM--QEELDAAQTKTT----VCDLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRIIFATLGVCIFYAFGFMVLPLFAYFIRDWRMLLLALTVPGVLCGALWWFIPESPRWLI
J., Tamai I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                            Tsuji A.;
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557
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22.7%;
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Pred. No. 8.6e-10;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
W -> G (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
    Yabuuchi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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      Hashimoto N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Chen J., Conway S.J., Ganapathy V.; Chen J., Conway S.J., Ganapathy V.; Chen J., Conway S.J., Ganapathy V.; Chen J., Conway S.J., Ganapathy V.; Chen J., Conway S.J., Ganapathy V.; Chen J., Conway S.J., Ganapathy V.; Chen J., Conway S.J., Ganapathy V.; Chen J., Conway S.J., Ganapathy V.; Chen J., Conway S.J., Ganapathy V.; Chen J., Conway S.J., Ganapathy V.; Chen J., Conway S.J., Ganapathy V.; Chen J., Conway S.J., Ganapathy V.; Chen J., Che
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nikaido H., Sai Y., Koizumi A., Shoji Y., Takada G., Matsuishi T.,
Yashino M., Kato H., Ohura T., Tsujimoto G., Hayakawa J., Shimane M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deficiency: a novel Arg169Gln mutation and a recurrent Arg282ter mutation associated with an unconventional splicing abnormality.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burwinkel B., Kreuder J., Sch
Gerbitz K.-D., Kilimann M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu X., Huang W., Prasad P.D., Seth P., Rajan D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Primary systemic carnitine deficiency is caused by mutations in gene encoding sodium ion-dependent carnitine transporter."; Nat. Genet. 21:91-94(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang N.L., Ganapathy V., Wu X., Hui J., Seth P., Yuen P.M., Wanders R.J., Fok T.F., Hjelm N.M.;
"Mutations of OCTN2, an organic cation/carnitine transporter, lead to deficient cellular carnitine uptake in primary carnitine deficiency.";
Hum. Mol. Genet. 8:655-660(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of two novel mutations in OCTN2 of three patients with systemic carnitine deficiency.";
hum. Genet. 105:157-161(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaz F.M., Scholte H.R., Ruiter J., Hussaarts-Odijk L.M.,
Rodrigues Pereira R., Schweitzer S., de Klerk J.B.C., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 261:484-487(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Carnitine transporter OCTN2 mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Two novel missense mutations of the OCTN2 gene (W283R and V446F) in patient with primary systemic carnitine deficiency."; Hum. Mutat. 15:118-118(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mayatepek E., Nezu J., Tamai I., Oku A., Katsura M., Shimane M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organic cation transport function and the carnitine transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mutations in novel organic cation transporter (OCTN2), an org
cation/carnitine transporter, with differential effects on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION OF VARIANT CDSP LEU-478, AND MUTAGENESIS. MEDLINE=20026865; PubMed=10559218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT CDSP LEU-478.
MEDLINE=99172075; PubMed=10072434;
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                                                                                                                                                                                                                 Hum. Mutat.
                                                                                                                                                                                                                                           carnitine transport activity."; Hum. Mutat. 15:238-245(2000).
                                                                                                                                                                                                                                                                                                     Wang Y., Kelly M.A., Cowan T.M., Longo N.; "A missense mutation in the OCTN2 gene associated with residual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20081068; PubMed=10612840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS CDSP ARG-283 AND PHE-446
                                                                                                                                                                                                                                                                                                                                                                   VARIANT CDSP LYS-452.
MEDLINE-20145665; PubMed=10679939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 274:33388-33392(1999).
                                                                                                                                                                                    FUNCTION: SODIUM-ION DEPENDENT, HIGH AFFINITY CARNITINE TRANSPORTER. ALSO TRANSPORTS ORGANIC CATIONS WITHOUT THE
DISEASE: DEFECTS IN SLC22A5 ARE THE CAUSE OF SYSTEMIC PRIMARY
                                                          TISSUE SPECIFICITY: STRONGLY EXPRESSED IN KIDNEY, SKELETAL MUSCLE.
                         HEART AND PLACENTA.
                                                                                             SUBCELLULAR LOCATION: Integral membrane protein
                                                                                                                             CARNITINE.
                                                                                                                                                    INVOLVEMENT OF SODIUM. INVOLVED IN THE ACTIVE CELLULAR UPTAKE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu X., Huang W., Leibach F.H., Ganapathy V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schweitzer S., Vorgerd M., Gempel K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Klerk J.B.C., Waterham H.R.,
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Matches
                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                            MUTAGEN
109 EQESCLDGWEFSQDVYLSTIVTEWNLVCEDDWKAPLTISLFFVGVLLGSFISGQLSDRFG 168
                                                                                                                                                                                                                                                                                                             VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                            61
                                                                                     59
                                                                                                                                                                              Local Similarity
                                                                                                               4
                                                                                                                               3 FEELLSQVGGLGRFQMLHLVFILPSLMLLIPH----ILLENFAAAIPGHRCWVHMLDN-NT 58
               DTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR-- 169
                                                   AWRNHT------VPLRLRDGREVPHSCRRYRLATIANFSALGLEPGRDVDLGQL
                                                                            GSGNETGILSEDALLRISIPL---DSNLRPEKCRRF---VHPQWQLLHLN-GTIHSTSEA 111
                                                                                                      YDEVTAFLGEWGPFQ--RLIFFLLSAS-IIPNGFTGLSSVFLIATPEHRCRVPDAANLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATION SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. ORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYOPATHY OR CARDIOMYOPATHY.
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                                                                                                                                                                                                                              557 AA;
                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                          352
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193
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                                                                                                                                                                                                                              62751 MW;
                                                                                                                                                                                                                                                                                                                                    452
                                                                                                                                                                                                                                                                                                                                                               446
                                                                                                                                                                     13.8%; Score 193.5; DB 1
22.0%; Pred. No. 1.3e-09;
                                                                                                                                                              37;
                                                                                                                                                                                                                                      M->R: LOSS OF BOTH CARNITINE AND ORGANIC CATION TRANSPORT FUNCTIONALITIES.
                                                                                                                                                                                                                                                                                       E -> K (IN CDSP).
/FTId-VAR_009256.
P -> L (IN CDSP; LOSS OF CARNITINE TRANSPORT BUT STIMULATED ORGANIC CARNITINE PROPERTY OF TRANSPORT BUT STIMULATED ORGANIC CARNITINE PROPERTY OF TRANSPORT BUT STIMULATED ORGANIC CARNIT
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                                                                                                                                                                                                                                                                                                                                              V -> F (IN CDSP).
/FTId=VAR_009255.
                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_009253.
W -> R (IN CDSP).
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Y -> C (IN CDSP).
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InterPro; IPR003663; Sugar_transporter.
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transmembrane; Sugar_transport; Transport; Glycoprotein;

MIM; 138160;

EMBL; J03810; AAA59514.1;

A31318; A31318

or send an email to license@isb-sib.ch).

Multigene family; Polymorphism

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A FURNMOTO H., Seino S., Imura H., Sieno Y., Eddy R.L., Fukushima Y.,

A Byers M.G., Seino S., Imura H., Sieno Y., Eddy R.L., Fukushima Y.,

Byers M.G., Shows T.B., Bell G.I.;

"Sequence, tissue distribution, and chromosomal localization of mRNA

"Tence of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
GTR2_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose
(Glucose transporter type 2, liver).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver, and Kidney; MEDLINE=88289735; PubMed=3399500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 NIRMVTIMSIMLWMTIS 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTESTINE, AND KIDNEY. SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSPORTER SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            524 AA
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                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
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Query Match
Best Local 9
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                                                                                                                                                                 GTR2_MOUSE STANDARD; PRT; 523 AA.
p14246; Q9DBA7;
01-JAN-1990 (Rel. 13, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter,
                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                (Glucose transporter type 2, liver). SLC2A2 OR GLUT2 OR GLUT-2.
                                                                  SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-90098776; PubMed-2602116;
                                                                                                                                       Mus musculus (Mouse).
                                                                                                         NCBI_TaxID=10090
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                           Suzue K.,
                                                                                                                                                                                                                                                                                                                                                                      149 QFLLLTGMLVGGIIG-----GHVSDRWLV------ESARWLIITNK 183
          STRAIN-C57BL/6; TISSUE-Liver
                                        Nucleic Acids
                                                                                                                                                                                                                                                                                                                              184 LDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAA -- QTKTTVCDLFRNPSMRKR 241
MEDLINE=89366666; PubMed=2771649;
                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        304 ILVALML 310
                                                Sequence
                                                                                                                                                                                                                                                                                                             LDEEVKAKQSLKRLRGYDDVTKDIN-----EMRKEREEASSEQKVSIIQLFTNSSYRQP 303
                                                                                                                                                                                                                                                                                                                                                   QLAIVTGILISQIIGLEFILGNY-DLWHILLGLSGVRAILQSLLLFFCPESPRYLYI--K 249
                                                                                                                                                                                                                                                                                         ICILVEL 248
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                       Lodish H.F., Thorens B.; of the mouse liver glucose transporter."; cids Res. 17:10099-10099(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                           524
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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359
368
389
400
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433
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4 (POTENTIAL)
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3 (POTENTIAL).
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1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                    Score 100; DB Pred. No. 0.23;
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6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
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5 (POTENTIA:
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2 (POTENTIAL).
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12 (POTENTIAL).
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DA600577207EC083 CRC64;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Kingwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Liver; MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 384-496 FROM N.A.

MEDLINE-92111400; PubMed-1765007;
Hogan A., Heyner S., Charron M.J., Copeland N.G., Gilbert D.J.
Jenkins N.A., Thorens B., Schultz G.A.;
"Glucose transporter gene expression in early mouse embryos.";
Development 113:363-372(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Differential screening of a PCR-generated mouse embryo cDNA library: glucose transporters are differentially expressed in early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith D.E., Gridley T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Development 116:555-561(199)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    postimplantation mouse embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                  FINGTION. FACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM LIKELY MEDIATES THE BIDIRECTIONAL TRANSFER OF GLUCOSE ACROSS THE PLASMA MEMBRANE OF HEPATOCYTES AND IS RESPONSIBLE FOR UPTAKE OF GLUCOSE BY THE BETA CELLS; MAY COMPRISE PART OF THE GLUCOSE-SENSING MECHANISM OF THE BETA CELL. MAY ALSO PARTICIPATE WITH THE NA(+)/GLUCOSE COTRANSPORTER IN THE TRANSCELLULAR TRANSPORT OF GLUCOSE IN THE SMALL INTESTINE AND KIDNEY.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: IN EMBRYO, EXPRESSED IN ENDODERM LAYER OF YOLK SAC AND LIVER PRIMORDIUM.
                                                                                                                                                                                                                                                                                                                                                                                  TRANSPORTER SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acids Res. 17:6386-6386(1989).
                                                                                                                                                                                                                                                                                                                                                                                                       BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copeland N.G., Gilbert D.J.,
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EMBL; X16986; CAA34855.1; -. EMBL; X15684; CAA33719.1; -. EMBL; S77926; AAB20847.1; -. EMBL; AK005068; BAB23792.1; -. use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrained the European Bioinformatics Institute. \$06920; \$06920 \$05319; \$05319 MGI:1095438; Slc2a2. There are no rest restrictions EMBL outstation a collaboration g

IPR003663; Sugar_transporter

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RESULT 6
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Matches
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                                                Q9QZ82;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cytochrome P450 11A1, mitochondrial precursor (EC 1.14.15.6) (CYPXIA1)
(P450(scc)) (Cholesterol side-chain cleavage enzyme) (Cholesterol
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                   Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                        CYP11A OR CYP11A1.
NCBI_TaxID=10090;
                                                                                                                           C11A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                 297 ANYROPILVALML 309
                                                                                                                                                                                                                                                                186 ALGTLHQLALVTGILISQIAGLSFILGN-QDHWHILLGLSAVPALLQCLLLLFCPESPRY 244
                                                                                                                                                                                                                                                                                     143 SLKSVVQFLLLTGMLVGGIIG-----GHVSDRWLV--------ESARW 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                       LYI--KLEEEVRAKKSLKRLRGTEDVTKDIN-----EMKKEKEEASTEQKVSVIQLFTD
                                                                                                                                                                                                     PSMRKRICILVFL 248
                                                                                                                                                                                                                                          LIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQT--KTTVCDLFRN 235
                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                 Conservative
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32
98
119
127
                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                   432 P
57106 MW;
                                                                                                                                                                                                                                                                                                                         6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transport; Transport; Glycoprotein;
                                                                                                                                                                                                                                                                                                             ; Score 95; DB 1; Length 523;
; Pred. No. 0.65;
27; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                          2 (POTENTIAL).
CYTOPLASMIC (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 (POTENTIAL).
CYTOPLASMIC (F
                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                          12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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8 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
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9 (POTENTIA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                  F12B5376CBDB5F63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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                                                                                                                           526 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose
(Glucose transporter type 2, liver).
SLC2A2 OR GLUT2 OR GLUT-2.
                                                                                                                                                                                        GTR2_RAT
P12336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:88582; Cyp11a
InterPro; IPR001128; Cyp11a
Pfam; PF00067; p450; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanaka M., Hennebold J.H., Adashi E.Y.;
Submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: CATALYZES THE SIDE-CHAIN CLEAVAGE REACTION OF
CHOLESTEROL TO PREGNENOLONE (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: Cholesterol + reduced adrenal ferredoxin +
                                                                                                                                                                                                                                                                                                                                                                                                                       228 TVCDL-FRN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steroidogenesis; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; Monooxygenase; Membrane; Heme; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ferredoxin + H(2)0.
-i- PATHWAY: INITIAL RATE-LIMITING REACTION IN THE SYNTHESIS VARIOUS STEROID HORMONES.
                                                                                                                                                                                                                                                                                                                                                              394 TVNDLVLRN 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 -WDLRQKRDFSQYPGVLYSLLGGNKLPFKNIQANITEMLAGGVDTTSMTLQWNLYEMAHN 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 MFHTSVPMLNLPPDFFRLLRTKTWKDHAAAWDVIFNKADE-----YTQNFY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: mitochondrial.-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 LLHLNGTI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 VHMLDNNTGSGNETGILSEDALLRISIP------LDSNLRPEKCRRFVHPQWQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKVQEMLRAEVLAARRQAQGDMAKMVQLVPLLKASIKETLRLHPISVTLQ------RY 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KWDL---VCDYQSLKSVVQFLL-------LTGMLVGGIIGGHVSDRW-LVESARW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIITNKLDEGLKALRKVARTNGIK------NAEETLNIEVVRSTMQEELDAAQTKT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHRRIKQQNSGNFSGVISDD-LFRFSFESISSVIFGERMGMLEEIVDPE-AQRFINAVYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P00189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                   STANDARD;
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22.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 93.5; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRION (BY SIMILARITY).
CYTOCHROME P450 11A1.
HEME (BY SIMILARITY).
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                                                                                                                                                                                                             522 AA
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                                                               transporter, member 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89;
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δÃ В Qy 밁

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transporter present in liver, intestine, kidney, and beta-pancreatic islet cells.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 55:281-290(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89003066; PubMed=3048704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thorens B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00083;
                                                                                                                                                                                                                                                                                                                                                                                                                                            pIR; A31556; A31556.
InterPro; IPR003663; Sugar_transporter.
InterPro; IPR003662; sub_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J03145; AAA41298.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chorens B., Sarkar H.K., Kaback H.R., Lodish H.F.,
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                  Multigene family.
                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Sugar transport; Transport; Glycoprotein;
                                                                                           TRANSMEM
                                                                                                       DOMAIN
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SEQUENCE
                          DOMAIN
                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIATES THE BIDIRECTIONAL TRANSFORTER. THIS ISOFORM LIKELY MEDIATES THE BIDIRECTIONAL TRANSFER OF GLUCOSE ACROSS THE PLASMA MEMBRANE OF HEPATOCYTES AND IS RESPONSIBLE FOR UPTAKE OF GLUCOSE BY THE BETA CELLS; MAY COMPRISE PART OF THE GLUCOSE-SENSING MECHANISM OF THE BETA CELL. MAY ALSO PARTICIPATE WITH THE NA(+)/GLUCOSE COTRANSPORTER IN THE TRANSCELLULAR TRANSPORT OF GLUCOSE IN THE SMALL INTESTINE AND KIDNEY.

SUBCELLULAR LOCATION: INTESTINE AND KIDNEY.

TISSUE SPECIFICITY. DEPCENDED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: PRESENT IN LIVER, INTESTINE, KIDNEY AND BETA-PANCREATIC ISLET CELLS.
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSPORTER SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                       PR00171
                                    186
207
216
237
237
302
323
338
359
366
402
402
402
403
                                                                                                                                                                                                                                                                                                                                                                                                                     sugar_tr; 1.
1; SUGRTRNSPORT
                                                                               10
31
197
117
117
1156
1146
1156
1156
1177
1185
206
206
203
203
203
301
337
337
338
338
338
442
442
442
442
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugar_transporter.
  57085 MW;
                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
2 (POTENTIAL).
  N-LINKED (GLCNAC. . .) (P
075AB81E56CF33F7 CRC64;
                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                         CYTOPLASMIC
                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                               CYTOPLASMIC
5 (POTENTIA)
                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
4 (POTENTIAL).
                                                                                                                                                                                                                                                                                   CYTOPLASMIC
3 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                               10 (POTENTIAL)
CYTOPLASMIC (P
                                                                                                                                    CYTOPLASMIC
                                        EXTRACELLULAR (POTENTIAL)
12 (POTENTIAL)
                             CYTOPLASMIC (POTENTIAL).
                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                   11 (POTENTIAL)
                                                                                                                                                                                                                                                                                     (POTENTIAL
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                                                                                (POTENTIAL).
                                                                                                                                      (POTENTIAL).
                  (POTENTIAL).
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Query Match

6.6%;

Score

DВ

Length 522;

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IN FKBX_MOUSE
IN FKBX_MOUSE
IN FKBY_MARC
Q61576
D7 30-MAY
D7 16-CC7
RR SIMEK
RR SIMEK
RR SIMEK
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RR SIMEK
RR STRAIN
RA SIMEK
RR STRAIN
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RR STRAIN
RR SEQUEN
RC Chrome
RI Genomi
RN [2]
RN [2]
RN [2]
RN HEDLIT
RA COSS b
TOOM
ROUSE
RF Charac
RI J. Bic
CC -i- FI
CC -i- S
CC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
65 kDa FK506-binding protein precursor (EC 5.2.1.8) (FKBP65) (FEBPRP)
(Peptidyl-prolyl cis-trans isomerase) (PPiase) (Rotamase)
(Immunophilin FKBP65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FKBX_MOUSE
Q61576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coss M.C., Winterstein D., Sowder R.C. II, Simek S.L.;
"Molecular cloning, DNA sequence analysis, and biochemical characterization of a novel 65-kba FK506-binding protein (FKBP65).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-JB6; TISSUE-Epidermis;
MEDLINE-94117013; PubMed-7507077;
Simek S.L., Kozak C.A., Winterstein D., Hegamyer G.,
"Sequence and localization of a novel FK506-binding p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKBP6 OR FKBP1-RS OR FKBP-RS OR FKBPRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome 11
                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96094328; PubMed=7493967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 18:407-409(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
MGD; MGI:104769; Fkbp6.
InterPro; IPR002048; EF-hand.
InterPro; IPR000886; ER_target
                                                                                         EMBL; L07063; AAC37678.1; -. HSSP; P20081; 1YAT.
                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN SYNTHESIS.

CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIG1. Chem. 270:29336-29341(1995).
FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQT--KTTVCDLFRN 235
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                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNYROPIVVALML 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4 FKBP-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: GLYCOSYLATED AND PHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN, BUT NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY CYCLOSPORINE A.
                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                        the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                              and the EMBL outstation
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GTR3_CHTCK STANDAKU;

P28568;

01-DEC-1992 (Rel. 24, Created)

01-DEC-1992 (Rel. 24, Last sequence update)

01-MAR-2002 (Rel. 41, Last annotation update)

Solute carrier family 2, facilitated glucose transporter, member
"Differential regulation of glucose transporter isoforms oncogene in chicken embryo fibroblasts."; Mol. Cell. Biol. 11:4448-4454(1991).
                                         SEQUENCE FROM N.A. MEDLINE-91342646; Pubmed=1875932; White M.K., Rall T.B., Weber M.J.;
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                 CHICK
                                                                                                NCBI_TaxID=9031;
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CARBOHYD
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PROSITE; PS00454; FKBP_PPIASE_2; 1.
PROSITE; PS50059; FKBP_PPIASE_3; 4.
PROSITE; PS00014; ER_TARGET; 1.
                                                                                                                                                                                                                                                                                                          131 ----GLIPPDATLYFDVVLLDVWNKADTVQS 157
                                                                                                                                                                                                                                                                                                                                  195 ARTNGIKNAEETLNIEVVRSTMQEELDAAQT 225
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                                                                                                                                                                                                                                                                                                                                                                              137 LVCDYQSLKSVVQFL--LLTGMLVGGIIGGHVSDRWLVESARWLIITNKLDEGLKALRKV 194
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                                                                                                                                                                                                                                                                                                                                                       -----AIVVGVGRLITGM-DRGLMGMCVNER-----RRLIVPPHLGYGSIGVA-- 130
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                                                                                                                                                                                                                                                                                                                                                                                                          -PRACPREVQMGDFVRYHYNGTFE------DGKKFDSSYDRSTLV---
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Calcium-binding.
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EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
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65 KDA FK506-BINDING
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FKBP-TYPE 2.
FKBP-TYPE 3.
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RESULT 10
GYRB_THEMA
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Best Local Similarity
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                           GYRB_THEMA P77993;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                      195 ARTNGIKNAEETLNIEVVRSTMQEELD--AAQTKTTVCDLFRNPSMRKRICILVFLR 249
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InterPro; IPR003663; Sugar_transporter.
InterPro; IPR003663; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTENSPORT.
PRINTS; PR00171; SUGRTENSPORT.
                                                                                                                                                228 QKLRGTQDVSQDI-----SEMKEESAKMSQEKKATVLELFRSPNYRQPIIISITLQ
                                                                                                                                                                                                                                        185 WPLLLGFTIVPAVLQCVALL---
                                                                                                                                                                                                                                                                       135 WDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRWLVESARWLIITNKLDEGLKALRKV 194
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PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Sugar transport; Transport; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M37785; AAA48662.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. PROBABLY A NEURONAL GLUCOSE TRANSPORTER.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSPORTER SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                     496 AA;
                                                                                                                                                                                                                                                                                                                           Conservative
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66
87
95
116
126
                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54174 MW;
                                                                                                                                                                                                                                                                                                                       6.2%; Score 86.5; D) 26.5%; Pred. No. 3.4; tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 (POTENTIAL)
CYTOPLASMIC (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (F
; 75B3C0F6la7A92A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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8 (POTENTIAL).
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5 (POTENTIAL)
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2 (POTENTIAL).
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                                          636
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                                          ₽
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                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999).

HATTORY DIA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE
INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
DNA RINGS, INCLUDING CATEMANUS AND KNOTTED RINGS.

-!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., "Byidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
DNA 9yrase subunit B (EC 5.99.1.3) (Topoisomerase II subunit B).
GYRB OR TOP2B OR TM0833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=MSB8 / DSM 3109;
MEDLINE-97017137; PubMed-8863738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermotoga maritima.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99287316; PubMed-10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00986; DNA_gyraseB_C; 1.
Pfam; PF00204; DNA_topoisoII; 1.
Pfam; PF02518; HATPase_C; 1.
Pfam; PF01751; Toprim; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U49692; AAC44498.1; -. EMBL; AE001750; AAD35915.1;
                                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                        SMART; SM00387; HATPASE_C; 1.
SMART; SM00433; TOP2C; 1.
PROSITE; PS00177; TOPOISOMERASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                 ProDom;
                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0418; TPI2FAMILY.
                                                                                                                                                                             (somerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ipaud O., Labedan B., Forterre P.;
gyrB-like gene from the hyperthermophilic bacterion Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 TETRAMER. SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P06982; 1AJ6.
TM0833; -.
                                                                                                                                                                                                                                                                                      PD149633; DNA_gyraseB_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermotogales; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001241; DNA_topoisoII.
IPR003594; HATPase_c.
IPR004359; HIS_KIN_sig.
IPR002936; Toprim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR002288; DNA_gyraseB_C
                                                                                                                  Topoisomerase; ATP-binding; Complete proteome
152 152 V -> M (IN REF. 1).
636 AA; 72427 MW; B21E0E0CBEC6F89E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / DSM 3109;
84.5;
No. 7;
                             DB 1;
                          Length 636;
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Best Local Similarity

6.0%;

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DOMAIN

Query Match

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GTR3_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-to carrier family 2, facilitated glucose transporter, member 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLC2A3 OR GLUT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P58352;
01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTR3_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                          "Expression of glucose transporters amongst ruminants.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     development
                                             Transmembrane; Sugar transport; Transport; Glycoprotein;
                                                                                 prosite; ps00216; sugar_transport_1; 1.
prosite; ps00217; sugar_transport_2; 1.
                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                          Augustin R., Navarrete-Santos A., Fischer B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                rissuE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Augustin R., Fischer B.; "Glucose transporter expression during bovine preimplantation embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Glucose transporter type 3, brain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 VIHIKRTEKVKTKNGEDEVIVEIAFQYTDSYSEDIVSFANTIKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 V---ARTNGI--KNAEETLNIEV----VRSTMQEELDAAQTKTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 DILEHRLREIAFLVPGLKIEFEDRINGEKKTFKFDGGIVEYVKY-----LNRGKKALHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 HSTSE-ADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 385-494 FROM N.A.
                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 VGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGSGNETGILSE
                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
                                                                                                                                                                                                                                                                                                            TRANSPORTER SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                           GLUCOSE TRANSPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LLLTGMLVGGI------IGGHVS----DRWLVESARWLIITNKLDEGLKALRK 193
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                                                                                                                     AF308829;
                                                                                                                                     AY033938; AAK70222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                     AAK63202.1; -
26
64
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 I (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                    CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                    PROBABLY A NEURONAL
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RESULT
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Best Local
MEDIINE-97392487; PubMed-9250701;
Currie M.J., Bassett N.S., Gluckman P.D.;
"Ovine glucose transporter-1 and -3: cDNA partial sequences and developmental gene expression in the placenta.";
                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member 3
(Glucose transporter type 3, brain).
SLC2A3 OR GLUT3 OR GLUT-3.
                                                        TISSUE=Placenta;
                                                                                                      Bennett B.L., Prosser C.G., Grigor M.R., "Isolation of cDNAs and tissue specific expression of ovine glucose transporters.";
                                                                                                                                      STRAIN=COOPWORTH;
MEDLINE=96109471; PubMed=8653093;
                                                                                                                                                                                         Ovis aries (Sheep).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
                                                                  SEQUENCE OF 88-248 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
                                                                                        Biochem. Mol. Biol. Int. 37:9-16(1995)
                                                                                                                                                                                                                                                                                                                                                      SHEEP
                                                                                                                                                                    SEQUENCE FROM N.A.
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CYTOPLASMIC (POTENTIAL)
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Pred. No. 6.3;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
PWEIV -> SLVYC (IN REF. 2).
EC42A3C648CAD23C CRC64;
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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3 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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DOMAIN
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                                                                                                                                                                                                                                                                135 WDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRWLVESARWLIITNKLDEGLK-ALRK 193
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EMBL: U89030; AAB49313.1; ...
InterPro; IPR003663; Sugar_transporter.
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGERTRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                 229 LWGTEDVAQDIQEMKDESMRMSQEKQV-----TVLELFRAPNYRQPIIISIMLQ
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-!- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. PROBABLY A NEURONAL GLUCOSE TRANSPORTER.
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-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
                                                                                                                                                                                                                                                                                                                                                           Local
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     STANDARD;
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54194
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Cytochrome P450 11A1, mitochondrial precursor (EC 1.14.15.6) (CYPXIA1)
(P450(Sec)) (Cholesterol side-chain cleavage enzyme) (Cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITINE-96244421; PubMed-8645627;
MEDITINE-96244421; PubMed-8645627;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
"Molecular cloning and nucleotide sequences of cDNA clones of sheep and goat adrenocortical cytochromes P450scc (CYP11A1).";
J. Steroid Biochem. Mol. Biol. 57:179-185(1996).
-!- FUNCTION: CATALYZES THE SIDE-CHAIN CLEAVAGE REACTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D50058; BAA08776.1; -. HSSP; P00189; 1SCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capra hircus (Goat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                desmolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Monooxygenase; Membrane; Heme; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00067; p450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steroidogenesis; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
373 VPLLKASIKETLRLHPISVTLQ 394
                                                                                                                                                                                                                                                   261 KTWR-DHVAAWDTIFNKAEKYTE-----IFYQDLRQKTEFRNYPGIL-YHLLKSEKMLL
                                                                                                                                                                                                                                                                                                                                                                           204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SSUE=Adrenal cortex;
                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   34 HILLENFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVH 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Cholesterol + reduced adrenal ferredo O(2) = pregnenolone + 4-methylpentanal + oxidized adrenal ferredoxin + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: mitochondrial. SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: INITIAL RATE-LIMITING REACTION IN THE SYNTHESIS VARIOUS STEROID HORMONES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHOLESTEROL TO PREGNENOLONE.
                                                                                                                                                                        -----LITGMLVGGIIGGHVSDRW-LVESARWLIITNKLDEGLKALRKVARTNGIK----
                                                                                                                                                                                                                                                                                                       PQWQLLHLNG--TIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFL 151
                                                                                                                           EDVKANITEMLAGGVDTTSMTLQWHLYEMARSLNVQEMLREEVLNARRQAEGDISKMLQM
                                                                                                                                                                                                                                                                                                                                                                        HFAFESITNVMFGER--LGMLEDTVNTEAQKFIDAVYKMFHTSVPL-LNLPPELYRLFRT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00385; P450.
; PS00086; CYTOCHROME_P450; 1.
                                                             ---NAEETLNIEVVRSTMQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001128; Cyt_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461
520 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 nu;
60418 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOCHROME P450 11A1.
HEME (BY SIMILARITY).
; 4FB09A3C89310317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 83.5; DB 1; Length 520; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ferredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
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                                                                                                                                                                                                                                                          312
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GRESULT
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RNN | M
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P46896;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wagstaff P., Kang H.Y., Mylott D., Robbins P.J., White M.K.; "Characterization of the avian GLUT1 glucose transporter: differential regulation of GLUT1 and GLUT3 in chicken embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Glucose transporter type 1) (GT1). SLC2A1 OR GLUT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=96157892; PubMed=8589457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00083; sugar_tr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L07300; AAB02037.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003663; Sugar_transporter.
InterPro; IPR003662; sub_transporter.
    DOMAIN
                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein. Localizes primarily at the cell surface (By similarity). SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE TRANSPORTER SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Biol. Cell 6:1575-1589(1995).

FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM MAY BE RESPONSIBLE FOR CONSTITUTIVE OR BASAL GLUCOSE UPTAKE. HAS A VERY BROAD SUBSTRATE SPECIFICITY; CAN TRANSPORT A WIDE RANGE OF ALDOSES INCLUDING BOTH PENTOSES AND HEXOSES (BY SIMLLARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00216; SUGAR_TRANSPORT_1; 1. PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family
    Sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SUGRTRNSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUGAR_TRANSPORT_2; 1.
gar transport; Transport; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                           11
32
32
32
115
115
146
                                                                                                                                                                                                                                                                                                                                                                                      2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
1 (POTENTIAL).
                                                                                                                  EXTRACELLULAR (POTENTIAL)
8 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
9 (POTENTIAL).
                                                                                                                                                                                                               CYTOPLASMIC
7 (POTENTIA)
                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL) 6 (POTENTIAL).
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5 (POTENTIA)
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2 (POTENTIAL).
                          CYTOPLASMIC (F
    EXTRACELLULAR (POTENTIAL)
                                                                                             EXTRACELLULAR
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Best Local
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             DOMAIN
                                      TRANSMEM
                                                                 DOMAIN
                                                                                       TRANSMEM:
                                                                                                             Repeat; Transmembrane;
                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                          Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT
                                                                                                                                                                                                                                                                                                                       EMBL; AF051139; AAC63975.1; -. EMBL; Z81312; CAB03595.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V., Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HIGH-AFFINITY GLUCONATE TRANSPORTER.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomyce
                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High-affinity gluconate transporter ght3 (Hexose transporter 3). GHT3 OR SPACIF8.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helland S., Radovanovic N., Hoefer M., Winderickx J., Lichtenberg "Multiple hexose transporters of Schizosaccharomyces pombe."; Bacteriol. 182:2153-2162(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHT3_SCHPO
Q92339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20200352; PubMed=10735857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 LRGTTDVSSDLQEMK-EESRQMMREK-----KVTIMELFRSPMYRQPILIAIVLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 VARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 WDLVCDYOSLKSVVQFLLLTGMLVGGIIGGHVSDRWLVESARWLIIT-NKLDEGLKALRK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                         PS00216; SUGAR_TRANSPORT_1; 1.
PS00217; SUGAR_TRANSPORT_2; 1.
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IPR003662; sub_transporter.
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Sugar transport; Transport; Glycoprotein.
CYTOPLASMIC (POTENTIAL).
1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Pred. No. 7.7;
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CYTOPLASMIC (POTENTIAL)
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230 EIIQT-NFNTIKSDI--EIEMAGGKARWIEIF-GKDIRYRTCLGFLVMLFREL 278
                    202 NAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICI--LVFLRKKI 252
                                                 185 NMLWGI---LLMVGVL----
                                                                                          137 EVAPPQIRGAVVATYQ-----IFSTGAALVAACINMGTHKLRKTAS-----WRTSFGI 184
                                                                                                                 82 NLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDY 141
                                                                                                                                         95 VYIIAELLLV-----TAVPS---WIQVLVGKILAGVGIGALSV-----LSPGYQS 136
                                                                                                                                                                 22 VFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISIPLDS 81
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22.3%;
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Pred. No. 8.9;
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EXTRACELLULAR (POTENTIAL)
12 (POTENTIAL).
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7 (POTENTIA
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4 (POTENTIAL).
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5 (POTENTIA
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11;

Search completed: July 1, 2002, 11:43:04 Job time: 214 sec

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C;Species: Caenorhabditis elegans
C;Species: Cot.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, December 1996
A; Reference number: 219573
A; Accession: T22509
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession:
                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:283228; PIDN:CAB05732.1; GSPDB:GN00019; CESP:F52F12.1
A;Experimental source: clone F52F12
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                                                                                                                                                                                                                                                           17 EDEVLEOVGNYGTYQIVEEFTICLPTSLPSAFSAFNID-----FVVGNPPHTCHI---- 66
                                                                                                                                             169 KFGRRRSFFVILTVLIVCGTASSFAKDIESFIILRFFTGLAFPALFQIPFIICMEFMGNS 228
                                                                                                                                                                                                                      67 ---PEGKE-----YLR---PLTNDTQILSCKQYNETQINVFR----AFTSAPVDTYS 108
                                                                                                                                                                                                                                        56 NNTGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADT-- 113
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                                                                                                                           169 ------LVESARWLII 180
                                                                                     181 TNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTT-----VCDLERN 235
                                                                                                        229 GRIESGLMISLEFGAAMALLGVVAMEIRRWROLIEFCNADFAEYIIYYFFLPESPRWSVS 288
                                                                    289 VGKWADAKKOLKKIAKMNGKSN----VDVDELVDSMKNHQNAAEEKETKRSHNVTDLEKT 344
                                345 PNLRRKTLIVTYI 357
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19.6%; Pred. No. 1.6e-09;
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A;Cross-references: DDBJ:AB017260; NID:g3869208; PIDN:BAA34399.1; PID:g3869209
                                                                                      A; Molecule type: mRNA
A; Residues: 1-557 <SEK>
                                                                                                                                                                  high-affinity carntine transporter, CT1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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A:Experimental source: placenta
C:Comment: This transporter functions in the elimination of cationic drugs and other xen
             Local Similarity
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A:Molecule type: mRNA
A:Mostdues: 1-557 <WUA>
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Best Local Similarity 22.0%; Score 193.5; DB 2; Length 557;
Matches 83; Conservative 37; Mismatches 106; Indels 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organic cation transporter protein 2 - human
N.Alternate names: OCTN2
C.; Species: Homo sapiens (man)
C.; Accession: JW0089 #sequence_revision 10-Jul-1998 #text_change 28-May-1999
                                                                                                                                                                                                                                                                                          339 NIRMVTIMSIMLWMTIS 355
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                                                                                                                                                                                                                                                                                                                                            289 RFEEAEVIIRKAAKANGI----
                                                                                                                                                                                                                                                                                                                                               183 KLDEGLKALRKVARTNGIKNAEETLNIEVVRST-----MQEELDAAQTKTTVCDLERNP 236
                                                                                                                                                                                                                                                                                                                                                                       229 IFSTLGVCIFYAFGYMVLPLFAYFIRDWRMLLVALTMPGVLCVALWWFIPESPRWLISQG 288
                                                                                                                                                                                                                                                                                                                                                                                                  170 -----WLV-ESARWLITTN 182
                                                                                                                                                                                                                                                                                                                                                                                                                          169 RKNVLFVTMGMQTGFSFLQIFSKNFEMFVVLFVLVGMGQISNYVAAFVLGTEILGKSVRI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 ----- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 EGESCLDGWEFSODVYLSTÍVTEWNLVCEDDWKAPLTISLFFVGVLLGSFISGOLSDRFG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 DTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR-- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AWRNHT------VPLRLRDGREVPHSCRRYRLATIANFSALGLEPGRDVDLGQL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 GSGNETGILSEDALLRISIPL---DSNLRPEKCRRF---VHPOWQLLHLN-GTIHSTSEA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 YDEVTAFLGEWGPFÓ--RLIFFÉLISAS-IIPNGFTGLSSVÉLIATPEHRCRVPDAANLSS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X.; Prasad, P.D.; Leibach, F.H.; Ganapathy, V. em. Biophys. Res. Commun. 246, 589-595, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 FEELLSQVGGLGRFQMLHLVFILDSLMLLIPH---ILLENFAAAIPGHRCWVHMLDN-NT 58
           13.7%;
Score 193; DB 2;
Pred. No. 3.9e-09;
                                                                                                                                                                                                                                                                                                                      -----VVPSTIFDPSELQDLSSKKQQSHNILDLLRTW 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function, and genomic organization of human OCTN2, a
     Length 557;
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;469-485/Domain: transmembrane #status predicted <TM10>F;494-514/Domain: transmembrane #status predicted <TM11>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;184-171/Domain: transmembrane #status predicted <TM2>
F;178-197/Domain: transmembrane #status predicted <TM2>
F;243-260/Domain: transmembrane #status predicted <TM3>
F;267-283/Domain: transmembrane #status predicted <TM4>
F;350-366/Domain: transmembrane #status predicted <TM4>
F;380-398/Domain: transmembrane #status predicted <TM5>
F;406-425/Domain: transmembrane #status predicted <TM7>
F;406-425/Domain: transmembran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-342,'N',344-556 <GOR>
A; Cross-references: EMBL: X78855, NID: 9633621; PIDN: CAA55411.1; PID: 9633622
C; Keywords: 91 ycoprotein; phosphoprotein; transmembrane protein
F; 20-46/Domain; transmembrane #status predicted <TMI>
TMINE THE PROPERTY OF THE PROPERTY OF TMINE PROPERTY OF T
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A;Reference number: S78533
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A: Residues: 1-556 <GRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organic cation transport protein OCT1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 550862; #sequence_revision 17-Jul-1998 #text_change 05-Nov-1999
C;Accession: 550862; $78533; I58089
R;Gruendemann, D.; Gorboulev, V.; Gambaryan, S.; Veyhl, M.; Koepsell, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: I58089; MUID:95082907

A:Molecular S50862
109 SIVANRSQLPLGPCEHGWVYDTP--GSSTVTEFNLVCGDAWKVDLFQSCVNLGFFLGSLV 166
                                                                                     103 GTIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGII 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: EMBL:X78855; NID:g633621; PIDN:CAA55411.1; PID:g633622
                                                                                                                                                                               62 CGWSQAEELNYTVPGLGPSDEASFLSQ--CMRYEV--DWNQSTLDC---VDP-----LS 108
                                                                                                                                                                                                                                                                    50 --WVHMLDNN-----TGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLN 102
                                                                                                                                                                                                                                                                                                                                                              5 DDVLBÓVGEFGWFQKQAFLLLCLÍSASLAPIYVGÍVFLGFT---PGHYCQNPGVABLSQR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 EELLSQVGGLGREQ---MLHLVFILPSLMLLIPHILLENFAAAIPGHRC------ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 RWLVESARWLIITNKLDEGLKALR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 EQLEQENCLDGWEYNKDVFLSTIVTEWDLVCKDDWKAPLTTSLFFVGVLMGSFISGQLSD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 SEADTEDCVDGWVYDQSYFESTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSD 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 LSSAWRNH-----SIPLETKDGRQVPQSCRRYRLATIANFSALGLEPGRDVDL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 NNTGSGNETGILSEDALLRISIPL---DSNLRPEKCRRF---VHPQWQLLHLN-GTIHST 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 YDEVTAFLGEWGPFO--RLIFFILSAS-IIPNGFNGMSIV---FLAGTPEHRCLVPHTVN 57
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organic cation transporter protein 2 - rat C;Species: Rattus norvegicus (Norway rat) c;pate: 10-Sep-1996 #sequence_revision 18-Oct-1996 #text_change 05-Nov-1999 C;Accession: JC4884 R;Okuda, M.; Saito, H.; Urakami, Y.; Takano, M.; Inui, K. Biophys. Res. Commun. 224, 500-507, 1996 A;Title: cDNA cloning and functional expression of a novel rat kidney organic cation tra A;Reference number: JC4884; MUID:96295517 A;Accession: JC4884; MUID:96295517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: DDBJ:DB3044; NID:g1502282; PIDN:BAA11754.1; PID:d1012421; PID:g1502
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A; Residues: 1-593 <OKU>
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hypothetical protein ZK455.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 ARWLIITNKLDEGLKALRKVARTNG-IKNAEETLNIEVVRSTMQEELDAAQTKT-TVCDL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 FRNPSMRKRICILVFL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 EFVGSGYRRTTAILYQMAFTVGLVGLAGVAYAIPDWRWLQLAVSLPTFLFLLYYWFVPES
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                                                                                                                                  342 PQIRKHTLILMY 353
                                                                                                                                                                                                                                                                                                                 228 FVGLGYRRMVGICYQIAFTVGLLILAGVAYVIPNWRWLQFAVTLPNFCFLLYFWCIPESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 TIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIG 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHVSDR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWSQAEELNYTVPGLGPSDEASFLSQ--CMRYEV--DWNQSTLDC---VDP-----LSS 109
                                                                                                                                                                               PSMRKRICILVF 247
                                                                                                                                                                                                                         RWLISQNKIVKAMKIIKHIAKKNG-----KSVPVSLQNLTPDEDA-GKKLKPSILDLVRT 341
                                                                                                                                                                                                                                                                      RWLIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRN 235
                                                                                                                                                                                                                                                                                                                                                                                                        GYLADREGRKECLLVTILINAISGALMAISPNYAWMLVFRELQGLVSKAGWLIGYILITE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAADRNQLPLGPCEHGWVYNTP--GSSIVTEFNLVCAHSWMLDLFQSVVNVGFFIGAMMI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDILEHIGEFHLFQ--KQTFFLLALLSGAFTPIYVGIVFLGFTPDHHCWSPGAAKLSQRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------VHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRREVHPQWQLLHLNG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.6%;
ilarity 18.3%;
Conservative 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 162.5; DB 2
Pred. No. 2.1e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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submitted to the EMBL Data Library, November 1995 A; Reference number: Z20432 A; Accession: T27870
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C;Accession: T27870
R;White, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL: 266567; PIDN: CAA91492.2; GSPDB: GN00028; CESP: ZK455.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-794 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Map position: V
A; Introns: 12/2; 6
A; Note: T08B1.1
                                                                                                                                                                                                                       R;Henkhaus, J.; Wohldmann, P.; Leimbach, D. submitted to the EMBL Data Library, August 1999 A;Description: The sequence of C. elegans cosmid T08B1 A;Reference number: Z20926
                                                                                                                                                                                                                                                                                                          sugar transport protein homolog T08B1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 29-Oct-1999
C;Accession: T30895
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                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-591 <HEN>
                                                                     C; Genetics:
                                                                                                              A;Cross-references: EMBL:AF039039; PIDN:AAB94177.2
                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                  A; Accession: T30895
                                                                                       A; Experimental source: strain Bristol N2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 VKDMNATGKINRCKE-----WEYDTSVMDRTIVTEWNRVCDNNWSRAHVHMSYSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 NEESFSA-ELGYTNYTWDQVLNSTIAFPRTFNKQRNELHHDQCHYFERDYVHIKLSPWAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 FEEDDLGILQLIGGCSYWQI--IVYLIISVQ-QVPHAMF-NLSVVYMMYQPDHWCKIPFF 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442 LYFLPESPRWLILNNKTKQAEKIIREACHYN---KSRLPSDLGLVRHAEKKKWMKHNEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 YLVGCFVGGFISDRYGRKTAITGFGILTMLFGFLLTYSKEFEIFLVVRFLLAATNEAADL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 MLVGGIIGGHVSDRW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 SYFHLFRSSELRFRNVVL 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 TVCDLFRNPSMRKRICIL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---LVESARWLIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLHLN--GTIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAYVLCMEVTGTKYRSIVGSLIQAPWACGYAFLALIAYLTKSWTMIHLICVLLHIISLML 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNNTGSGNETGILSE--DALLR--ISIPLDSN-----LRPEKC----RREVH----PQWQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                           62/1; 89/1; 111/3; 145/3; 325/2; 359/1; 468/2; 540/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone ZK455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 156; DB 2;
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170
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189 KALEKVARTNG 199 291 VIEKIARUNG 301 291 VIEKIARUNG 301 291 VIEKIARUNG 301 291 VIEKIARUNG 301 292 VIEKIARUNG 301 293 VIEKIARUNG 301 294 VIEKIARUNG 301 295 VIEKIARU
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7.3%; Score 103; DB 2; Length 745; imilarity 18.2%; Pred. No. 0.53; Conservative 44; Mismatches 112; Indels 168; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; 160/3; 205/3; 249/3; 293/2; 350/1; 386/3; 462/3; 546/2; 669/3; 680/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rotein K05F1.6 - Caenorhabditis elegans
norhabditis elegans
-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                      DAAQTKTTVCDLFRNPSMRKR---ICILVFL 248
                                                                                                                IPESPRWLMVQNRVSEAEEVIRKACREPPFPFNMCTTSKCGNLPSDLELVSHRER 457
                                                                                                                                                          LVESARWLIITNKLDEGLKALRKVAR-----TNGIKNAEETLNIEVVRST 215
                                                                                                                                                                                                                                       TLCMEITGTKYRAMVGSMLQAPWALGYALLALIAYLTKSWKTIQVIAAGLHFMSI 397
                                                                                                                                                                                                                                                                                                                                                           GCVLGGIASDKIGRKPTIIGFGILSSMLGVFLPFNDYYPMFLLIRLLSAICNEAA 337
                                                                                                                                                                                                                                                                                                                                                                                                                        GGIIGGHVSDR------ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      )T----NDTTISSHGPYLWGVDDIKNISFVFPNANSDGAYQRDSCYFYERSEERYRQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTGSGNETGILSE-----DALLRISIPL----DSNLRPEKCRRFVHPQWQLLH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIIGGCRWWQI--WIYVLIALQ-QIPHAMFNLNVVYMMYDPEFQCMVPGF----- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQVGGLGRFQMLHLVFILPSLMLLIPHILLE-----NFAAAIPGHRCWVH 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            he EMBL Data Library, June 1995
The sequence of C. elegans cosmid K05F1
mber: Z18537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGFLSLPLMAYLERKSWRNLYRIISFLPLGYAVCLLPFAYESPRWLLVKGRNKEAM 290
NGG--KIGFLDLFTMKELRYRTISVCI-VFM 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LETAMSEAWKDVAPKKKC-QAYHFEKDVMVETIVTDFNLVCDSWFAKGHAHMFYS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nces: EMBL:U29377; NID:9868173; PID:9868176; PIDN:AAA68713.1; CESP:K05F source: strain Bristol N2
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>: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GTIHSTSEADTEP----CVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLL 153
                                                                                                                                                                                                                                                                                                    ---- 170
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A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ ac.uk/Projects/C_elegans/ ac.uk/Projects/ ac.uk/Projects/C_elegans/ ac.uk/Projects/ ac.uk/Projec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-447 <STO>
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
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A;Cross-references: GB:J03810; NID:g187133; PIDN:AAA59514.1; PID:g307125 C;GenetCos: A;Gene: GDB:SLC2A2; GLUT2
A;Cross-references: GDB:I19995; OMIM:138160
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C:Superfamily: glucose transport protein
C:Keywords: transmembrane protein
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Best Local
                                                                                                                                    181 KSRLPSDLGLVRHAEKKKWMKHNEKPSYFHLFRSSELRFRNVVL 224
                                                                                                                                                                                                                   202 NAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICIL 245
                                                                                                                                                                                                                                                                                                   124 LIAYLTKSWTMTHLICVLLHIISLMLLYFLPESPRWLILNNKTKQAEKIIREACHYN--- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 TIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 LTYSKEFEIFLVVRFLLAATNEAADLAAYVLCMEVTGTKYRSIVGSLIQAPWACGYAFLA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 ILVALML 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 LDEEVKAKQSLKRLRGYDDVTKDIN-----EMRKEREEASSEQKVSIIQLETNSSYRQP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 LDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAA--QTKTTVCDLFRNDSMRKR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 QLAIVTGILISQIIGLEFILGNY-DLWHILLGLSGVRAILQSLLLFFCPESBRYLYI--K 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 OFLLLTGMLVGGIIG-----GHVSDRWLV--------ESARWLIITNK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 ICILVFL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 TIVTEWNRVCDNNWSRAHVHMSYSLGYLVGCFVGGFISDRYGRKTAITGEGILTMLEGFL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZK455.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 7.0%; Score 98.5; DB 2; Length 447; Similarity 17.4%; Pred. No. 0.71; 39; Conservative 22; Mismatches 52; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      ------LVESARWLIITNKLDEGLKALRKVARTNGIK 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 111;
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L-arabinose transport (permease) araE - Bacillus subtilis
C;Beccies: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: F69587
C;Accession: F69587
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
R; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yasta, K.; Yoshida
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A; Accession: F69587
A; Status, Tralinians, M.; Millishida, M.; Masuda, A.; Schillishida, M.; Masuda, A.; Schillishida, A.; Considerium Saddie, M.; Millishida, A.; Considerium Saddie, M.; Millishida, A.; Considerium Saddie, M.; Wata, K.; Yoshida
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Schillishida, M.; Millishida, M.; Millishi
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-105,'D',107-180,'T',182-326,'T',328-350,'F',352-431,'P',433-523 <ASA>
A;Cross-references: EMB:X15884; NID:g51090; PIDN:CAA33719.1; PID:g51091
R;Hogan, A; Heyner, S; Charron, M.J.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.;
Development 113, 363-372, 1991
                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X16986; NID:g55511; PIDN:CAA34855.1; PID:g55512 R;Asano, T.; Shibasaki, Y.; Lin, J.L.; Akanuma, Y.; Takaku, F.; Oka, Y. Nucleic Acids Res. 17, 6386, 1989
A;Title: The nucleotide sequence of cDNA for a mouse liver-type glucose transporter p A;Reference number: S05319; MUID:89366666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-523 <SUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Mus musculus (house mouse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 24-Sep-1999
C:Accession: S06920; S05319; B44887; I48367
R:Suzue, K.; Lodish, H.F.; Thorens, B.
Nucleic Acids Res. 17, 10099, 1989
A:Title: Sequence of the mouse liver glucose transporter.
A:Reference number: S06920; MUID:90098776
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A;Experimental source: strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 KVARTING-----IKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICIL 245
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A; Note: sequence extracted from NCBI backbone (NCBIN:77926, NCBIP:77927)
R; Waeber, G.; Thompson, N.; Haefliger, J.A.; Nicod, P.
J. Biol. Chem. 269, 26912-26919, 1994
A; Title: Characterization of the murine high Km glucose transporter GLUT2 gene and its A; Reference number: A55078; MUID:95014557
A; Accession: I48367
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-5 <RES>
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A;Residues: 384-431,'p',433-496 <HOG>
A;Cross-references: GB:S77926; NID:g242129; PIDN:AAB20847.1; PID:g242130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable membrane transporter [imported] - Arabidopsis thaliana (5.5pecies: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C;Accession: G94864 C;Accession: G94864 R;Lin, X.; Kaul, S.; Rounslev. S n. Shaa m. . . .
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C;Superfamily: glucose transport protein
C;Keywords: liver; transmembrane protein
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C;Genetics:
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C; Superfamily: glucose transport protein
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A; Residues: 1-521 <STO>
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Best Local :
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Best Local Similarity
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                          181 THKLDEGLKALRKVARTNGIKNAEETLHIEVVRSTMQEELDAAQTKTTV--CDLFRNPSM 238
                                                                                                                                        125 SYEPSTIVTK----WDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRWLVESARWLII 180
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Local Similarity 25.6%;
                                                                                      188 SYLVNSAFTQVPGTWRWMLGVSGVPAVIQFILML---
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                                                                                                                                                                                                   6.6%; Score 93; DB: 26.9%; Pred. No. 2.6; ative 23; Mismatches
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                                                                                                                                                                                                            38; Indels
                                                                                                 ----FMPESPRWLFM 232
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glucose transport protein, hepatic - rat C.Species: Rattus norvegicus (Norway rat) C.Species: Rattus norvegicus (Norway rat) C.Pate: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 17-Nov-2000 C.Pate: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 17-Nov-2000 C.Pate: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 17-Nov-2000 C.Pate: 28-Feb-1990 #text_change 17-Nov-2000 F.Pate: 28-Feb-1990 #text_change 17-Nov-2000 F.Pate: 28-Feb-1990 #text_change 17-Nov-2000 F.Pate: 28-Feb-1990 #text_change 17-Nov-2000 F.Pate: 28-Feb-1990 F.Pate: 28-Fe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
A; Introns: 5/3; 36/3; 122/2; 164/1; 202/3; 257/1; 319/3; 354/3; 388/3; 456/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-246, 'K', 248-522 <AHN>
A; Cross-references: EMBL:L28134
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A; Residues: 1-522 <THO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 SLKSVVQFILLTGMLVGGIIG-----GHVSDRWLV------
                                                                                                                                                                                                    244 LYL--NLEEEVRAKKSLKRLRGTEDITKDIN-----EMRKEKEEASTEQKVSVIQLFTD 295
296 PNYRQPIVVALML 308
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Search completed: July 1, 2002, 11:41:47 Job time: 248 sec

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Result
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Human cDNA clone r	AAK93441	22	6	•	74	45	
cDNA 5'-end	17	22	6	•	74	44	
Human polynucleoti	AAI82398	22	596		79.4	43	
Mouse organic anio		22	1638	•	81	42	
organic ani	AAV79585	20	2171	•	81.8	41	
hOAT1	AAC85819	22	2127	•	81.8	40	
Human	AAZ29300	21	2123	10.2	81.8	39	
Human	AAI84356	22	379		85.2	38	
Rat organi	AAV79584	20	2294		88.2	37	
Rat li	AAA10196	21	280		88.8	36	
Human	AAL02433	22	419		98.2	35	
Human full-length	AAK94561	22	1871		108	34	
Human cDNA	AAK93534	22	789		108	<u>ω</u>	
	AAK92269	22	789		108	32	
Nucleotide	AAF55043	22	1316		130.8	31	
Rat EST-deriv	AAH98991	22	685			30	
Probe #24865 used	AAI56179	22	339			29	o
Probe #1724	AAI27308	22	339		•	28	o
Human bone m	AAK50227	22	339		•	27	a
Human brain e	AAK24178	22	339		•	26	o
	ABA40206	22	339	•	136.2	25	a
Human foetal	ABA75594	22	339		•	24	a
Human reprodu	AAL07075	22	9370		•	23	
Human reproc	AAL07074	22	447			22	
Probe	AAI43191	22	540		160.4	21	o
Probe #8107	AAI18174	22	540		160.4	20	a
Human bone m	AAK37346	22	540		160.4	19	O
Human brain exp	AAK11579	22	540	•	160.4	18	o
Probe #8860 f	ABA30394	22	540		160.4	17	Ω
Human foetal liver	ABA63144	22	540	٠	160.4	16	o
ani	AAF32614	22	2210		•	15	
Ξ.	AAD12607	22	2194		•	14	
transporter	AAD17480	22	2047			13	
0	1256	22	86	•		12	
transporter	174	22	2455	26.0	208.8	11	
Human polynucleoti	AA161001	22	μ	29.0		10	

ALIGNMENTS

AAZ38316 standard; cDNA; 804

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RESULT AAZ3 316 ID AAZ3 AX AAZ3 AX HUMBA XX HP02 KW Orga KW Gorga 
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Matches 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kato
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          domains. The cDNA was isolated from a human liver cell cDNA library, from tissue localisation studies has been found to be expressed only the liver. The protein has homology with the rat organic cation transporter (EMBL Accession No. V09945) which is involved in drug excretion, and may have a similar function. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors,
                                                                                                   encodes a
                                                                                                                                                                                Human proteins with transmembrane opposite ration and differentiation,
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 ligands and binding proteins, and as biologically
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                                                                                                                  represents the human cDNA clone HP02000 which
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                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
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; 2000US-0663870.
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J, Werhman T;
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Pred. No. 2.7e-241;
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genetic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiantammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibact
(HYSE-) HYSEQ INC
                                                                 03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875
                                                                                                                                                               05-FEB-2001; 2001WO-US03800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   naematopoiesis regulation; tissue growth; immunomodulator; ac inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic dis
                                                                                                                                                                                                                                                                                                                                                                                                                        antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; immunomodulator; activin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein homologue-encoding cDNA, SEQ ID NO:752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA08976 standard; cDNA; 1353
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Query Match Best Local Matches

Similarity

63.2%;

Score 508; DB 22; Pred. No. 6.2e-153; Mismatches

Length 1353; Indels

Conservative

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Gaps

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1 atggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcat 60

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Sequence 1353 BP; 349 A; 298 C; 315 G; 391 T; 0 other;

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cc haematopoiesis regulatory activity; tissue growth activity;
cc immunomodulatory activity; activity; activity;
cc immunomodulatory activity; activities; haemostatic, thrombotic or
cc thrombolytic activities; receptor or inhibin-related activities;
cc the involved in oncogenesis, cancer cell proliferation or metastasis.
cc Depending on their biological activities, polypeptides and nucleotides of
cc the invention are useful for preventing, treating or ameliorating medical
cc conditions, e.g., by protein or gene therapy. Such conditions include
cc cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
cc disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
cp of birns, bone disorders (e.g., osteoporosis), and abnormal
cc vascular growth. Polypeptides involved with tissue regeneration and
cc repair (or nucleic acids encoding them) may be used to promote wound
cc healing (e.g., of burns, incisions and ulcers), while those with
cc batterial and fungal infections in addition to immune disorders.
                                          Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention or have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane protein; transport; organic anion; splice variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; organic anion transporter; hOAT; liver; kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hOATS DNA
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                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2000; 2000WO-US18980
                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2001.
                                   transporter (hOAT) polypeptides. hOAT polypeptides are preferentially transporter that facilitate the transport of organic anions across the proteins that facilitate the transport of organic anions across the cell membrane. The mechanism of transport is thought to be a secondary corteritary active transport involving exchange of another organic anion. Or tertiary active transport involving exchange of another organic anion. HOAT2A and hOAT2B are thought to be splice variants as they are noward and hOAT2B are thought to be splice variants and the DNA identical except at the C-terminal end. hOAT proteins and the DNA identical except at the C-terminal end.
                                                                                                                                                                                                                                                                                                                   (META-) METABASIS THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                12-JUL-1999;
                                                                                                                                                                                                                                                                                          Sun W;
                                                                                                                                                                             Claim 1; Fig 6; 95pp; English
                                                                                                                                                                                                        useful in gene therapy procedures -
                                                                                                                                                                                                                     Nucleic acids encoding human organic anion transporter polypeptides,
                                                                                                                                                                                                                                                  P-PSDB; AAB47276
                                                                                                                                                   The sequences given in AAC85819-24 encode human organic anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tcamatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac
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                       diseases associated with inappropriate hOAT expression.
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                                                                                                                                                                                                                                                                                                                                                    99US-0143771.
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Sequence 2684 BP; 800 A; 533 C; 541 G; 810 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; peripheral nervous system; disease; Huntington's disease; haemostatic; halzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; chemokinetic;
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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                                                                              21-JAN-2000;
25-APR-2000;
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                                                                                                                                                                                                             26-JUL-2001
                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                        leukaemia; ss.
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     , 2000US-0488725.
; 2000US-0552317.
; 2000US-0598042.
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708 totcaatcactgacttcagtggctaaatttgtattcatggctggaatgatggtgggaggc
                                                            648 gtgtatgacagaatctccttctcatccaccatcgtgactgagtgggatctggtatgtgac 707
                                                                             361 gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressant and cytostatic activity. The polypoptide or polypucleotides are useful in gene therapy. A composition containing a polypoptide or polypucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous and central nervous system diseases, such as lateral sclerosis, and shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and shy-Drager Syndrome. Other uses include the activity, cancer diagnosis and thrapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                    468 gacaatgacactggggccctcagccaagatgcactcttgagaatctccatcccactggac 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                         288 atggcettteaggaeeteetgggteaegetggtgaeetgtggagatteeagateetteag 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1418; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                          ctgaatgggaccttccccaacacagtgacgcagacatggagccctgtgtgggatggctgg 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                actgcattcatacctggccatcgctgctgggtccacatcctggacaatgacactgtctct 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Zhou P,
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.7%; Score 335.2;
78.7%; Pred. No. 3e-
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Yang Y,
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AAD09561
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                                                                                                Human; transporter and ion channel-10; TRICH-10; cystic fibrosis; mood; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy, hypertension; angina; neurological disorder; asthma; bipolar disorder; plck's depression; Alzheimer's disease; epilepsy; vaccine; arrhythmia; huntington's disease; hental disorder; schizophrenia; hold; anxiety; stroke; muscule disorder; cardiomyopathy; cataract; myocarditis; drave's disease; muscular disorder; schizophrenia; polymyositis; dermatomyositis; diabetes mellitus; immunological disorder; psoriasis; sickle cell anaemia; wilson's disease; infertility; Cushing's disease; scheroderma; pulmonary artery stenosis; nootropic; addison's disease; malabsorption syndrome; hypercholesterolaemia; cancer; ss.
                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                 Human transporter and ion channel-10 (TRICH-10) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-2001 (first entry)
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WO200146258-A2. /*tag= /product= "Human TRICH-10 protein" Location/Qualifiers

YX YX PD XX PF YX PR PR PR 22-DEC-2000; 2000WO-US35095

23-DEC-1999; 14-JAN-2000; 21-JAN-2000; 28-JAN-2000; (INCY-) INCYTE GENOMICS INC ; 99US-0172000. ; 2000US-0176083. ; 2000US-0177332. ; 2000US-0178572. ; 2000US-0179758. ; 2000US-0181625.

Novel human transporter and ion channel proteins useful for treating P-PSDB; AAE04897. Baughn MR, Burford N, Hillman JL, Azimzai Y, 2001-418042/44. Khan FA; Au-Young J, Lu DAM, Yue H, Nguyen DB, Yang J, Yao MG,

Claim 5; Page 147; 160pp; English. preventing transport, neurological, muscle and immunological

PAN XXX PAN XX disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar The present sequence is transporter and ion channel-10 (TRICH-10) cDNA. TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Toth cystic fibrosis, Becker's muscular dystrophy. epilepsy, ischaemic cerebrovascular

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osteoarthritis; burn; incision; ulcer; periodontal disease; neuropathy; nervous system disease; bone growth; cosmetic plastic surgery; gut protection; gut regeneration; fibrosis; cancer;
                                                               Secreted
                                                                                                 cDNA encoding a human secreted protein.
                                                                                                                                           06-MAR-2001
                                                                                                                                                                                                                           AAC61892 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                          tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtggatggctgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gctgcagccattcctggtcatcgttgctgggtccacatgctggaccataatactggatct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400;
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                                                                                                                                                                                                                                                                                                                                                                                                     totoaatcactgacttcagtggctaaatttgtattcatggctggaatgatggtgggaggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctgaatgggaccttccccaacacaagtgacgcagacatggagccctgtgtggatggctgg
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                                                         protein; platelet disorder; stem cell disorder; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 335.2; DB 22; Length 1986; Pred. No. 3.7e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G; 528
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                                                                                                                                                                                                                                                                                                                                                                                           CC AAC61879-93 encode secreted human proteins. The secreted proteins are CC useful in assays to determine their biological activities. The proteins CC can also be used as biomarkers to identify tissues or cell types which CC express the proteins. The polynucleotide molecules can be used as CC The proteins and antibodies are useful in diagnosis and treatment of CC diseases associated with altered expression of these proteins. The CC discases associated with altered expression of these proteins are also useful for prevention or treatment of platelet CC disorders, stem cell disorders, osteoporosis or osteoarthritis, burns, CC incisions, ulcers, periodontal diseases, central and peripheral nervous CC system diseases and neuropathies, for healing fractured bones and to CC induce cartilage and/or bone growth in cosmetic plastic surgery. The CC proteins are also useful for gut protection or regeneration, for the CC treatment of lung or liver fibrosis, for stimulating blood cell CC generation in patients receiving cancer chemotherapy and for treatment of the marrow transplantation patients.
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel secreted human proteins useful for stimulating blood cell generation in patients receiving cancer chemotherapy, treating l marrow transplantation patients and for healing fractured bones
                                                                                                                                                                                                                                                                                                                                                                  Sequence 2027 BP; 530 A; 501 C; 459 G; 537 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2;
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20-AUG-1999;
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ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
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                                                                                                                                                                                                                                                                          Conservative
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99US-0150054
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Pred. No. 4.1e-96;
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                                                                                                           The sequences given in AAC65819-24 encode human organic anion transporter (hOAT) polypeptides. hOAT polypeptides are preferentially expressed in the liver and kidneys of humans. OAT's are membrane proteins that facilitate the transport of organic anions across the cell membrane. The mechanism of transport is thought to be a secondary or tertiary active transport involving exchange of another organic anion hOAT2A and hOAT2B are thought to be splice variants as they are identical except at the C-terminal end. hOAT proteins and the DNA
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   Sequence 1977 BP;
                                                                                            encoding them, may be used in the prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human organic anion transporter polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-1999;
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                                                       diseases associated with inappropriate hOAT
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DB; AAB47275.
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in; transport; organic anion; splice variant;
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   502 A; 491 C; 450 G;
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      534 T; 0 other;
                                                                                            treatment and diagnosis
                                                             expression.
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Best Local
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                     21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                               Human polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                   AAI61001 standard; cDNA;
                                                                                                                 26-DEC-2000;
                                                                                                                                             26-JUL-2001
                                                                                                                                                                         WO200153312-A1
                                                                                                                                                                                                                                                chemokinetic;
                                                                                                                                                                                                                                                                                                                                                             22-OCT-2001
                                                                                                                                                                                                                                 leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atggcctttcaggacctcctgggtcacgctggtgacctgtggagattccagatccttcag
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2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                 2000WO-US34263
                                                                                                                                                                                                                                              thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.1%;
77.3%;
                                                                                                                                                                                                                                                                                                                                 SEQ ID
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Pred. No. 2.2e-
                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                  4990.
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XIX
                                                                                                              RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 4990; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     utilisation of the activities such as: Immune system suppression, utilisation of the activity, chemotactic/chemokinetic activity, haemostatic activiny, hibbin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1132 BP; 274 A; 265 C; 285 G; 305 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.N.S disorders.
              10-DEC-2001
                                                 AAD17476;
                                                                                AAD17476 standard; cDNA; 2455
                                                                                                                                                                                                                                                                                                                                                                             147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
                                                                                                                                                                 327 catttatcagacaggt 342
                                                                                                                                                                                                                                                                                                                                                                                                                                              87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                            atccacagcacaagtgaggcagacacagaaccctgtgtgggatggctgggtatatgatcaa 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggggccctcagccaagatgcactcttgagaatctccatcccactggactcaaacatgagg 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggaatcetcagtgaagatgeectettgagaatetetateecaatagaeteaaatetgagg 252
                                                                                                                                                                                                                                                                                                    atotoottotoatocaccatogtgactgagtgggatotggtatgtgactotoaatoactg 266
                                                                                                                                                                                                                                                                                                                                                                        ttccccaacacaagtgacgcagacatggagccctgtgtggatggctgggtgtatgacaga 206
                                                                                                                                                                                                                                                                                                                                                                                                                                             ccagagaagtgtcgtcgctttgttcatcctcagtggcagctccttcacctgaatgggacc 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccagagaagtgtcgttcgttcgtccatccccagtggcagcttcttcacctgaatgggact 312
                                                                                                                                                                                    catgtctcagacaggt 508
                                                                                                                                                                                                                                   acttcagtggctamatttgtattcatggctggamtgmtggtgggaggcmtcctmggcggt 326
                                                                                                                                                                                                                                                   aaatcagtggttcaattcctacttctgactggaatgctggtgggaggcatcataggtggc 492
                                                                                                                                                                                                                                                                                                                          agctacttcccttcgaccattgtgactaagtgggacctggtatgtgattatcagtcactg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                  (first entry)
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Wehrman T, X
Goodrich R,
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, Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 232.8; DB 2
Pred. No. 2.7e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 1132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qian XB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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2 atggcattttctgaactcctggacctcgtgggtggcctgggcaggttccaggttctccag 61 1 atggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcat Matches

Conservative

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human transporter and ion channel-9 (TRICH-9) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-2000;
17-MAR-2000;
24-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; transporter and ion channel; TRICH-9; therapy; akinesia; cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastritis; inflammation; ss.
                                                                                                                 channels (TRICH-9) protein. The TRICH DNA, protein and their agonist and antagonists are useful in the diagnosis, treatment and prevention of transport disorders (akinesia, amyotrophic lateral sclerosis, cystic fibrosis), neurological (Alabeimer's disease, dementia, depression, epilepsy), muscle (e.g. cardiomyopathy, Becker's muscular dystrophy) or immunological disorders (e.g. allergies, acquired immunodeficiency syndrome (AIDS), Crohn's disease, rheumatoid arthritis, scleroderma, multiple sclerosis), viral, bacterial, parasitic, protozoal and helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Khan FA, Walia NK, Gandhi AR, Tribo
Thornton M, Greene BD, Hernandez R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-FEB-2001; 2001WO-US05942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200162923-A2.
                                                                                                                                                                                                                                                                                                                                  Thirteen human transporters and ion channels (referred to as TRICH-1 to TRICH-13), useful in the diagnosis, treatment and prevention of transport (e.g. akinesia), neurological, muscle or immunological disorders (e.g. allergies) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                   Claim 11; Page 127-128; 131pp; English.
                                                                                                                                                                                                                                                                    The present sequence is a cDNA encoding human transporters and ion
                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                     Sequence 2455 BP; 416 A; 842 C; 707 G; 490 T; 0 other;
                                                                                                       gastritis and inflammation.
        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-582050/65.
                                                                                                                                                                                                                                                                                                                                                                                                                     AAE10332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000US-0188333.
; 2000US-0190230.
; 2000US-0192077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0184866.
2000US-0187947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0193500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Human TRICH-9 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lal P,
            26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Policky JL, Nguyen DB, Au-You
hi AR, Tribouley CM, Patterson
             Score 208.8; DB 2
Pred. No. 2.3e-56;
Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borowsky ML,
                               DB 22; Length 2455;
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sanjanwala MS;
     0;
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     Gaps
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RESULT 12
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                                                                                                          06-JAN-2000;
06-JAN-2000;
11-JAN-2000;
03-FEB-2000;
WPI; 2001-418355/44
                            Kato S,
                                                                                             03-MAR-2000;
                                                                  (PROT-) PROTEGENE INC
                                                                                                                                                                          28-DEC-2000; 2000WO-JP09359.
                                                                                                                                                                                                                                  W0200149728-A2.
                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            contraceptive; antiinfertility; antiinflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                               cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease, cytostatic;
                                                                                                                                                                                                                                                                                                                                                                      Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; hydrophobic domain; gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD12566 standard; cDNA; 2865 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD12566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482 gctgcgtgcggccctgcctcagacaggt 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 atcataggtggccatgtctcagacaggt 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtctatgaccgcagcatcttcacctccacaatcgtggccaagtggaacctcgtgtgtgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     teteatgetetgaageceatggeeeagteeatetaeetggetgggattetggtgggaget 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein having hydrophobic domain encoding cDNA clone HP03613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cccaatgccacggccaccagctggagcgaggccgacacggagccgtgtgtgggatggctgg
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                                                  SAGAMI CHEM
                         Kimura T;
                                                                                                         2000JP-0000585.
2000JP-0000588.
2000JP-0002299.
2000JP-0026862.
                                                                                            2000JP-0058367
                                                                                                                                                                                                                                               /product= "Human protein having hydrophobic domain"
/note= "CDS is specifically is claimed in claim 3"
                                                                                                                                                                                                                                                                                                 Location/Qualifiers 338..2074
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                                                     RES CENT
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Query Match Best Local

Similarity

DB 22;

Length 2865;

Sequence 2865 BP; 488 A; 973 C; 830 G; 574 T; 0 other;

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The present sequence is human protein with hydrophobic domain encoding CC CDNA clone Hp03613. The polynucleotide and polypeptide of the invention CC associated with inappropriate polypeptide expression. The polynucleotides CC into a host cell and culturing the cell to express the protein. The CC polynucleotides and its complementary sequences may also be used as DNA CC probes in diagnostic assays and also used in gene therapy. The CC and in assays to identify modulators of polypeptide expression and CC and in assays to identify modulators of polypeptide expression and CC supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of Theumatoid arthritis and insulin dependent diabetes), to modulate complements to modulate tissue growth activity (e.g. for the cc disease), to modulate activin and inhibin activity (e.g. for the creatment of parkinson's disease, Huntington's disease and Alzheimer's cfertility), to modulate chemotactic and chemokinetic activity, to modulate receptor indulate haemostatic and thrombolytic activity, to modulate receptor to the turnour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 252-257; 563pp; English.
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818 gctgcgtgcggccctgcctcagacaggt 845
                     481 atcataggtggccatgtctcagacaggt 508
                                                                              421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc 480
                                                                                                                        698 gtctatgaccgcagcatcttcacctccacaatcgtggccaagtggaacctcgtgtgtgac
                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                 241 tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac
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                                                                                                                                                                                                                                                                                                                                                                                                               121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 atggcetttgaggagetettgagteaagttggaggeettgggagattteagatgetteat 60
                                                         gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
                                                                                                                                                                                                             ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtggatggctgg
                                                                                                                                                                                         cccaatgccacggccaccagctggagcgaggccgacacggagccgtgtgtgggatggctgg
                                                                                                                                                                                                                                                          gccagcatcctagggagcttgagtcctgaggccctcctggctatttccatcccgccgggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 187; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 208.8; DB 2
Pred. No. 2.5e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2000;
09-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; transporter and ion channel; TRICH-13; therapy; akinesia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human transporter and ion channel-13 (TRICH-13) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD17480 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastritis; inflammation; cardiant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                            The present sequence is a cDNA encoding human transporters and ion channels (TRICH-13) protein. The TRICH DNA, protein and their agonist and antagonists are useful in the diagnosis, treatment and prevention of transport disorders (akinesia, amyotrophic lateral sclerosis, cystic fibrosis), neurological (Alzheimer's disease, dementia, depression, epilepsy), muscle (e.g. cardiomyopathy, Becker's muscular dystrophy) or immunological disorders (e.g. allergies, acquired immunodeficiency syndrome (AIDS), Crohn's disease, rheumatoid arthritis, scleroderma, multiple sclerosis), viral, bacterial, parasitic, protozoal and helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-2001; 2001WO-US05942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thirteen human transporters and ion channels (referred to as TRICH-1 to TRICH-13), useful in the diagnosis, treatment and prevention of transport (e.g. akinesia), neurological, muscle or immunological disorders (e.g. allergies) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
                                                                                                                                               Sequence 2047 BP; 363 A; 655 C; 598 G; 431 T; 0 other;
                                                                                                                                                                                                            gastritis and inflammation.
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   Local Similarity
nes 312; Conserv
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, Walia NK,
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; 2000US-0187947;
; 2000US-0188333.
; 2000US-0190230.
; 2000US-0192077.
; 2000US-0193500.
Conservative
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                               22.5%;
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hi AR, Tribouley CM, Patterson
      0;
   Score 180.8; DB 22;
Pred. No. 2.2e-47;
0; Mismatches 187;
                                                                   DB 22;
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            Indels
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   06-JAN-2000;
06-JAN-2000;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell proliferation; immunomodulatory; autoimmune disorder; antimicrob multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostat Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; hydrophobic domain; gene therapy; nutritional supplement; cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein having hydrophobic domain encoding cDNA clone HP03882.
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                                                                                                                                         28-DEC-2000;
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       ; 2000JP-0000585.
; 2000JP-0000588.
; 2000JP-0002299.
                                                                                                                                         2000WO-JP09359
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 58..1710
                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "Human protein having hydrophobic domain"
/pote= "CDS is specifically is claimed in claim 3"
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supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arrhritis and insulin-dependent diabetes), to modulate treatment of parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling fertility), to modulate chemotactic and chemokinetic activity, to modulate and thrombolytic activity, to modulate receptor
409 gtctatgaccgcagcgtcttcacctccaccatcgtggccaagtgggacctggtgtgcagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional
                        361 gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2194 BP; 408 A; 710 C; 615 G; 461 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is human protein with hydrophobic domain encoding CDNA clone HP03882. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides into a host cell and culturing the cell to express the protein. The
                                                                                                                                                                                                 241 tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac 300
                                                                                                                                                                                                                                                              233 ----cggtttccacaaacatgacccccaaggcccttctgaccatctccatcccgccaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 527-532; 563pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAE06612
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03-MAR-2000; 2000JP-0058367.
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                                                                                      cccaatgccacggccaccagctggagcgaagctgacacggagccgtgtgtgggacggctgg
                                                                                                                                                                        ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity, to modulate inflammation and to inhibit tumour growth.
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Pred. No. 2.2e-47;
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                                                                                                                                                                                                      Matches 312;
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                                                                                                                                                                                                                                                                                                     The present sequence encodes a human placental organic anion transporter designated OAT4. OAT4 has nephrotrophic activity. The OAT4 protein and encoded gene are useful in studying causes of abnormality, including the application of a variant nucleic acid as a probe to detect the presence of a gene encoding the transporter OAT4, or to identify or quantify such gene, and in developing drugs to prevent or treat various kidney diseases and abnormal foetal growth.
                                                                                                                                                                                                                                                                           Sequence 2210 BP; 426 A; 709 C; 614 G; 461 T; 0 other;
           173
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 23-26; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Placental organic anion transporter gene and encoded polypeptide OAT4, useful in studying causes of abnormality, and in developing drugs to prevent or treat various kidney diseases and abnormal fetal growth -
               121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
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                                                                                                        61
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                                                                                                                                        53
                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                l atggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcat 60
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tcagccgccatcccaggccaccgatgctggacacacatgctggacaatggctctg----
                                                               gtgctcaccttcatcctcccctgcctcatgataccttcccagatgctcctggagaacttc
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Pred. No. 2.3e-47;
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ALIGNMENTS

	FEATURES SOUICE	JOURNAL MEDLINE COMMENT	AUTHORS	RESULT 1 AV652088 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE
/organism="Homo sapiens" /db_xref="taxon:9606" /clone="GLCCWF10" /clone_lib="GLC" /tissue_type="corresponding non cancerous liver tissue" /dev_stage="Adult" /lab_host="SOLR" /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"	Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai. Location/Qualifiers 1. 615 Cocaniformal Homo sanions"	with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001) 21625106 Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z. Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma	AV652088 AV652088 AV652088 AV652088 AV652088:1 GI:9873102 EST. BURATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 615)

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KEYWORDS
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC encurs generated during the R&D process and may have higher chance of
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Fujiyama,A., Hattori,M., Toyoda,A.,
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GSS; GSS (genome survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGACGTCCGCGGAGCTCTTGAGTCAAGTTGGAGGCCTTCGGAGATTTCAGATCCTTCAT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGCAGCCATTCCTGGTCATCGTTGCTGGGTCCACATGGTGGACAATAATACTGGATCT
 J., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin, Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilcon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392;
                                                                                                                                                                                                                                            AA680184 399 bp mRNA linear EST 19-DEC-
zillc10.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA
clone IMAGE:430482 3' similar to TR:G1293672 G1293672
KIDNEY-SPECIFIC TRANSPORT PROTEIN. ;, mRNA sequence.
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                 AA680184.1 GI:2656651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
160 c 154 g 207 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="PTB-106L08.F"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"
/db_xref="taxon:9598"
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                                                                                                                                                                                                                                  TGAGAAAAAAAATCTCAAGGAAAAGGCATAAAAATGATTGCTACACAAAAGTGACCAAA
                                                                                                                                                                                                                                                                                               CTGTGTGTGACTTGTTCCGCAACCCCAGTATGCGTAAAAGGATCTGTATCCTGGTATTTT
                                                                                                                                                                                                                                                                                                              ctgtgtgtgacttgttccgcaaccccagtatgcgtaaaaggatctgtatcctggtatttt
                                                                                                                                                                                                                                                                                                                                                             TAAAGGCACTTAGAAAAGTTGCACGCACAAATGGAATAAAGAATGCTGAAGAAACCCTGA
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BI338656
362506 MARC
BI338656
BI338656.1
EST.
Pig.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares_fetal_liver_spleen_1NFLS_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                     GI:15031939
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99.7%;
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                                                                cDNA 5', mRNA sequence
                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 399;
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Best Local 9
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                   421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc
                                                                                                                                                369
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les 390; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 atggcctttgaggagctcttgagtcaagttggaggccttggggagatttcagatgcttcat 60
                                                                                                                                                                                                                                                                                                                  ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
                                                                                                                                                                                                                                                                                                                                                                                         gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
TATCAGTCTCAGAAACCACTGGTCCAATTTGCATTCATGGCTGGAATGCTGCTGGGAGGC
                                                                                        gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat
                                                                                                                                                                   ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtgggatggctgg
                                                                                                                                                                                                                     TCAAACTTGAAGCCAGAGAAATGTCGGCGCCTACCTCCACCCCCAGTGGCAGCTCCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctggtttttattcttccctctcatgttattaatccctcatatactgctagagaacttt 120
                                                                                                                                                CTGAATGGAACCTTCCCCAATGTGACTGATCTGGACACGGAGCCCTGTGTGGACGGCTGG
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                                                                                                                                                                                                                                                                                                                                                                      ACAGCGGCCATTCCTGGTCATCACTGCTGGGTCCGCATCCTCGACAATGACACTGACTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGCTTTTGAGGAGCTCCTGAATGAAGTCGGTGGCTTGGGGAAATTCCAGATGCTTCAG
                                                                         GTGTATGACCAAAGCTCCTTCTCCCACCATCGTGACTGAGTGGGACCTCGTATGTGAT
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PO Box 166, Clay Center, NE
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stone, R.T., Heaton, M.P., and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 581)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 131 row: H column: 23 Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.7%; ilarity 76.8%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
163 c 136 g 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="pooled"
/lab_host="DH10B"
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Pred. No. 1.2e-
D; Mismatches
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Sus.
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                               tcataggtggccatgtctcagacaggtggctggtggaatctgctcggtggttgataatca 541
  TCATAGTTGCCCATGTCTCAGACAGTTGGCTGGTGGAATCTGCTCGGTGGTTGATAATCA 304
                                                                                                                                                                                                                      320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham
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367 bp mRNA linear EST 19-
zj20a06.sl Soares_fetal_liver_spleen_lNFLS_Sl Homo sapiens
clone IMAGE:450802 3' similar to TR:G1293672 G1293672
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4444 Forest Park Parkway,
Tel: 314 286 1800
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Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
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//lab_host="DHIOB (ampicillin resistant)"
//note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
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/db_xref="taxon:9606"
/clone="IMAGE:450802"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llni.gov
Plate: LLAM10958 row: o column: 18
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High quality sequence stop: 819.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:4972265"
/clone="IMAGE:4972265"
/clone="DHIOB (TI phage-resistant)"
/lab_host="DHIOB (TI phage-resistant)"
/note="organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 197 c 185 g 247 t
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/strain="FVB/N"
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73.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1054)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602109666F1 NCI_CGAP_Kidl4 Mus musculus cDNA clone IMAGE:4237793 5', mRNA sequence.
BF783752
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 665.
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                                                                              /Clone_lib="NCI_CGAP_Kid14"
//lab_host="DH10B (TI phage resistant)"
/lab_host="DH10B (TI phage resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally, Primer: Oligo dT
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 250 c 256 g 272 t
                                                                                                                                                                                                                              /clone="IMAGE:4237793"
                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
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Email: genome-res@gsc.riken.go.jp,
URL:hhtp://genome.gsc.riken.go.jp,
Carninci,p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, KIKEN Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-rel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
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241 tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac 300
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                                                                                                                                                                                              121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                                                                                                                                                                                                        145 ATGATATTTGTGTTAATCTGCCATGCCCTGTCGGCTCCTCACACTCTTTTGGAGAACTTC 204
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                                                        GATAATGGCAGTAGGATCCTGAGCCAAGATGACCTCCTGAGGATCTCCATCCCCCTGGAC 324
                                                                                        99taatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="kidney"
/dev_stage="0 day neonate"
/lab_host="DH10B"
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72.0%;
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61 ctggtttttattcttccctctctcatgttattaatccctcatatactgctagagaacttt 120
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                                                      ATGGCCTTTCAGGAACTCCTGAATCAAGTTGGAAGCCTAGGAAGATTCCAGATCCTTCAG 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail_nih.gov______
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://image.llnl.gov
Plate: LLAM11122 row
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 866)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5', mRNA sequence.
BI102429
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Mammalia; Eutheria; Rodentia;
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/clone=1ib="NCI_CGAP_Kid14"
/lab_host="DH10B_(T1_phage=resistant)"
/note="Drigan: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library.|"
a 206 c 189 g 268 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
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                                                                                                                                                                36.0%;
72.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 ATCTCTTTTGTTCTCCTCCTCGTAGGCCTTGTGGTACCTCATATTACAATGGAGAACTTT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481
                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                653 ATCATATGTGGCCATTTGTCAGACAGGTTG 682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCAGGCACTGAATTCTGTTGCTAAAATTTTCATTCATGATTGGCTATTTATAGGGGCT 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCAACCTGAGACTGGATAAATGTCGTCGTTTTGCCCCAACCACTGGCATCTTCTTCAT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGTATGACAGGAGCAACTTCCTTTCTACCATTGTGACTGAGTGGGACCTGGTGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 739)

1 (bases 1 to 739)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Person underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter, E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW107114.1 GI:6077914
                                                                                                                                                                                                                                                                                                 Fax: 314 A00 1018
Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This - _ _ _ _ info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Other_ESTs: um18h07.x1
                                                                                                                                                                                                                            High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nouse mouse.
                                                                                                                                                                                                                                                      primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                 314 286 1800
314 286 1810
/clone_lib="Sugano mouse kidney mkia"
/sex="female"
/dev_stage="adult"
                                                                                                                          /organism="Mus musculus"
/strain="C57BL"
                                                                             /db_xref="taxon:10090"
/clone="IMAGE:2192701"
                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                            BC016496
                                                                          SOURCE
                                                                                              KEYWORDS
                                                                                                                VERSION
                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 ATGTCCTTTCAAGAACTCCTGAATCAAGTTGGAAGCCTAGGAAGATTCCAGATCCTTCAG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 tcaaatotgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 gctgcagccattcctggtcatcgttgctgggtccacatgcttggaccaataatactggatct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 527 TTGAATGGCACTTTCTCCAATGTGTCAGAGCCAGACACTGAGCCCTGTGTGGATGGTTGG 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtgggatggctgg 360
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                                                                                                                                                                                                                                                                                                                                                                                               421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc 480
                                                                                                                                                                                                                                                                                                                                                                                                                                       587 GTGTATGACAGGAGCAACTTCCTTTCTACCATTGTGACTGAGTGGGACTTGGTATGTGAA 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ctggtttttattcttccctctctcatgttattaatccctcatatactgctagagaacttt 120
                                                                                                                                                                                                                                                                                      707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATAATGGCAGTAGGATACTGAGCCAAGATGACCTCCTGAGGATCTCCATCCCCCTGGAT 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTGCAGCCATTCCCAATCATCGCTGCTGGGTCCCCATCCTTGACAATGACACTGCCTCT 406
                                                                                                                                                                                                                                                                                    ATCATATGTGGCCATCTGTCAGACAGGT 734
                                                                                                                                                                                                                                                                                                                                                              TCTCANGCACTGAATTCTGTCACTAAATAATCATTGATTGGCCTATNNTATAGNGGT 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCAACCTGAGACTGGATAAATGTCGTCGTTTTGCCCAACCACAGTGGCATCTTCTTCAT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367;
                                                                                                                                                  BC016496 1914 bp mRNA linear HTC 05-NOV-200 Mus musculus, Similar to solute carrier family 22 (organic cation transporter)-like 2, clone IMAGE:4236791, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1914)
                                                                                                                BC016496.1 GI:16741330
                                                                              house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be used to isolate the cDNA insert. Size selec
performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.4%;
72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 284.8; DB 9
Pred. No. 8.7e-63;
0; Mismatches 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 t
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                                                                                                                                                                                                    HTC 05-NOV-2001
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REFERENCE

AUTHORS

Strausberg, R

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Best Local
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421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc 480
                                                                                                                                                           241 tcaaatotgaggccagagaagtgtcgttgtcgctttgtccatccccagtggcagcttcttcac 300
                                                                                                                                                                                                                                                                                                                  336 GATAATGGCAGTAGGATCCTGAGCCAAGATGACCTCCTGAGGATCTCCATCCCCCTGGAT 395
                                                                                                                                                                                                                                                                                                                                                                                                        276 ACTGCAGCCATTCCCAATCATCGCTGCTGGGCCCCCATCCTTGACAATGACACTGCCTCT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                 121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 ATCTCTTTTGTTCTCTTCCTCGTAGGCCTTGTGGTACCTCATATTACAATGGAGAACTTT 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 ATGGCCTTTCAGGAACTCCTGAATCAAGTTGGAAGCCTAGGAAGATTCCAGATCCTTCAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ctggttttttattcttccctctctcatgttattaatccctcatatactgctagagaacttt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 atggcetttgaggagetettgagteaagttggaggeettgggagattteagatgetteat 60
                                                                     gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
                                                                                                                                 TTGAATGGCACTTTCTCCAATGAGACAGAGCCAGACACTGAGCCCTGTGTGGATGGTTGG 514
                                              GTGTATGACAGGAGCAACTTCCTTTCTACCATTGTGACTGAGTGGGGACCTGGTGTGTGAA 574
                                                                                                                                                                                                                          TCCAACCTGAGACTGGATAAATGTCGTCG-TTTGCCCAACCACAGTGGCATCTTCTTCAT 454
                                                                                                                                                                                                                                                                                                                                           99taatgaaactggaatcetcagtgaagatgccctcttgagaatctctatcccactagac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov
Series: IRAK plate: 31 Row: e Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: villalon@bcm.tmc.edu.
villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (31-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV-SPORT6"
376 c 385 g 593 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:4236791"
/tissue_type="Kidney, normal.
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.2%;
73.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 283.2; DB 11; Length Pred. No. 2.5e-62; O; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 1914;
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481 atcataggtggccatgtctcagacaggt 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KONDO, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wastahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RÎKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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RIKIN Mouse ESTs (Arakawa, T., et al. 2001)

Uppublished (2001)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                  further details.
                                                                                                                                                                                                                                                                                                                                                                         Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,Y. and Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                         e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagama, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                         /clone_lib="RIKEN full-length enriched,
kidney"
/tissue_type="kidney"
/dev_stage="0 day neonate"
                                                                                                                                            /clone="D630003H14"
                                                                                                                                                                             /db_xref="taxon:10090"
                                                                                                                                                                                                          'organism="Mus musculus"
                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                             ACCESSION
                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 ATGGCCTTTCAGGACCTTATAATTCAAATTGGCAGCTTGGGGAGGTTCCAGATTCTTCAC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 gctgcagccattcctggtcatcgttgctgggtccacatgctggaccaataatactggatct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 ATGATATTTGTGTTAATCTGCCATGCCCTGTCGGCTCCTCACACTCTTTTGGAGAACTTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 ACTGCAGCCATTCCTAGTCATCGCTGCTGGGTCCCCATCCTTGACAATGACACTGCCTCT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 TCCAACCTGAGACCGGATAAATGCCGTCGCTATATTCAACCACAGTGGCATCTCCTTCAT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac 300
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                                                                                                                                                                                                                                                                                                                                                                                                 421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtgggatggctgg 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                    AI530049 974 bp mRNA linear EST 18-MAR-1:
ui88f01.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1889497 5' similar to TR:035956 O35956 RENAL ORGANIC ANTON
                                                                                                                     TRANSPORTER 1. ;, mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                AI530049.1 GI:4444184
                                       house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'lab_host="DH10B"
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                                                                                                                                                                                                                           183 taatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagactc 242
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                                                                              418 CAACCTGAGACTGGATAAATGTCGTCGTTTTGCCCAACCACAGTGGCATCTTCTTCATTT
                                                                                                                                                                                    358 TAATGGCAGTAGGATCCTGAGCCAAGATGACCTCCTGAGGATCTCCATCCCCCTGGATTC 417
303 gaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtggatggctgggt 362
                                                                                                           243 aaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcacct 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcatct 62
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
                                                                                                                                                                                                                                                                                         TGCAGCCATTCCCAATCATCGCTGCTGGCCCCCATCCTTGACAATGACACTGCCTCTGA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq primer: custom primer used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                             Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Salto, T., Kiyosawa, H., Yamanaka, I., Alzaw Hayashizaki, Y., Hara, A., Itoh, M., Kawal, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                     Email: genome resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                        Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                   421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc 480
                                                           361 gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
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AGAAGTGTCATCGCTTCCTCCACCCCCAGTGGCAGCTCCTTCACCTGAATAGGACCTTCG 293
                                                                           TCCTCAGCCCTGATGTCCTCCTGAGAATCTCCATCCCACTGGATTCAAACTTAAAGCCAG
                                                                                                                                                     GTCATCGCTGCTGGGTCTACATCCTGGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV605334
AV605334
5', mRNA
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AV605334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 29 (22), E108 (2001) 21570554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
and Sugimoto,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV605334.1 GI:9735707
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bovine ESTs
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was
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/note-"Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"
164 c 137 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="ElKI028B10"
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Pred. No. 3.2e-60;
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                                                                                                                                                     ----TAATGCCACTGAGA 173
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Search completed: July Job time: 9387 sec ۲, 2002, 14:44:48

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Maximum DB seq length: 2000000000
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804
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Listing first 45 summaries
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1 US-09-172-711-48
2 US-08-647-397-1
2 US-08-232-463-14
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3 US-09-913-320-1
3 US-08-65-65-178
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4 US-08-23-095-1
5 US-08-314-979-1
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5 PCT-US92-06840-1
5 US-09-541-782-9
5 US-09-541-782-9
5 US-09-141-000-4
5 US-08-316-611-3
5 US-08-565-655-3
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5 US-08-91-140-3
5 US-08-91-140-3
5 US-08-91-140-3
5 US-08-91-140-3
5 US-08-91-140-3
5 US-08-91-172-6
5 US-08-810-712-6
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                                                                        Sequence 48, Appl
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	Match Local nes 12 1 atg 1 atg 1 1 1 1 1 1 1 1 1	1 -711. NO. (e. 48, NO. (e. 48, NO. (e. 48, NO. (e. ANT: NANT: NANT: NANT: NANT: NANT: NANT: NO. 4 (e. 48, NISM: N		5000
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RAN	ore 88.8; Mismatch Mi	2,7	-376-8 -447-5 -453-6 -453-6 -185-3 -500-8 -174-6 -174-6 -1446-8 -1340-3 -461-3 -480-3 -483-3	555 55 55 55 55 55
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CORRESPONDENCE ADDRESS:

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RESULT 3
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                                                                                                                        Sequence 14, Application US/08232463 Patent No. 5670367
          GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 1:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: Mus musculus
                                                                                                                                                                                                                       523 TTGGAGGACCTGTGTTTGGAGAACTGTCAGACAGGT 558
                                                                                                                                                                                                                                                      473 tgggaggcatcataggtggccatgtctcagacaggt 508
                                                                                                                                                                                                                                                                                   413 tatgtgattatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctgg 472
                                                                                                                                                                                                                                                                                                                                                         409 ATGGCTGGATCT-----ACAACAGCACCAGAGACACCATTGTGACAGAGTGGGACTTGG 462
                                                                                                                                                                                                                                                                                                                                                                                    353 atggctgggtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctgg 412
                                                                                                                                                                                                                                                                                                                                                                                                                        349 TGCATCTGCCAAACGCCAGTCTTCCCAATGACACCCAGGGGGCCACCGAGCCATGCTTGG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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LENGTH: 2102 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/647,397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
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Pred. No. 2.5e-07;
0; Mismatches 88; Indels 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 5.8%; Score 46.6; DB 1; Length 7218; Best Local Similarity 5.7%; Pred. No. 6.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703)683-410
TELEX: 899149
INFORMATION FOR SEQ ID NO:
                               1124 RRRRRRRRRRRRRRRRRRRRRRRRR 1098
                                                                                           1484 TGTAATTACCTATCTATGCAAGTAGTTAAAGAGATAGAAGAATTTGGTACRRRRRRRRR 1425
                                                            775 aatgattgctacacaaaagtgaccaaa 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                          715 cgtaaaaggatctgtatcctggtatttttgagaaaaaaatctcaaggaaaaggcataaa 774
                                                                                                                                                                                             655 gagctggatgcagcacagaccaaaactactgtgtgtgacttgttccgcaaccccagtatg 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 tgtgattatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtg 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 91 114 300.6 FILLING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1800 Dia
CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                   ggaataaagaatgotgaagaaaccotgaacatagaggttgtaagatccaccatgcaggag 654
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APPLICANT: DORNER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CITY: Alexandria
STATE: VA
                                                                                                                                                      141 tcgttgctgggtccacatgctggacaataatactggatctggtaatgaaactggaatcct 200
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                           261 gtgtcgtcgctttgtccatccccagtggcagcttcttcacct 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 9
FILING DATE: 26-AUG-1991
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                                                                                                                                                                                                                                                                                    21 gagtcaagttggaggccttgggagatttcagatgcttcatctggtttttattcttccctc 80
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                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703)683-4109
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                           4.5%; Score 36; DB 1; Length 7218; 6.4%; Pred. No. 0.19;
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US-07-906-871-15/c
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; LOCATION:
US-07-906-871-15
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION NUMBER: PCT/US89/03051
APPLICATION NUMBER: 1000
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                           FEATURE
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.2830004
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                                                               LOCATION:
                                                                                                             LOCATION:
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                                                                                                                                                                                                           LOCATION:
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                                                                               NAME/KEY:
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SYSTEM: PC-DOS/MS-DOS
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9745..16396
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9597..9744
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18-JAN-1991
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                                                                               Matches
                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                 TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gonsalves, Dennis
APPLICANT: Meng, Baozhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
7764 GGCTGAATGGCAAGTCAAATTGGGAAACTCCCCGGTGAATCAAATGAGGCTTTTGAAGCC 7823
                                                                                                                                                                                TOPOLOGY: 15
MOLECULE TYPE:
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                   559 ggcttaaaggcacttagaaagttgcacgcacaaatggaataaagaatgctgaagaaacc 618
                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60 FILING DATE: 17-DEC-1997 ATTORNEY/AGENT INFORMATION: NAME: GOLdman, Michael L. REGISTRATION NUMBER: 30,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 20-MAY-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 60/047,147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                        Local Similarity 50.0%;
                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                         83; Conservative
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                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                              30,727
                                                                Score 33.2; DB 3; Length 8743; Pred. No. 1.7; 0; Mismatches 83; Indels 0
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Patent No. 5997878 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-658-665-178
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                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212)840-0712
INFORMATION FOR SEQ ID NO:
2083 AAAGCTGTAGATTTTTCCAGAATGGATATTAAGGGAGATGATATTAGCAAAATGGGAATA 2142
                                                                                                                                                        1964 AAGAAGATTTAGTAAACGAATTAATTGAAAATACCAATAGTTTCGAAGATATAATGACTA 2023
                                                                                                                                                                                                                                       1904 AATTGGTAGACAGAAAAATATTATCTAAACCAGATACGTCTAAAACAGAAATAGAGATTA 1963
                                                                             2024 TACCTACCAGTATCCCTATGAGATA-TTTTTTTAAACCGGTACTAAGAGAAAAAGTATCT 2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Frommer Esq., William S. REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45431
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)840-3333
                                   728 gtatcctggtatttttgagaaaaaaatctcaaggaaaaggcataaaaatgattgctaca 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/658,665
                                                                                                                  668 cacagaccaaaactactgtgtgtgacttgttccgcaaccccagtatgcgtaaaaggatct 727
                                                                                                                                                                                   608 ctgaagaaaccctgaacatagaggttgtaagatccaccatgcaggaggaggtggatgcag 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Paoletti, Enzo
APPLICANT: Pincus, Steven E.
APPLICANT: Cox, William I.
APPLICANT: Kauffman, Elizabeth K.
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Recombinant Poxvirus TITLE OF INVENTION: Compositions and Uses NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7884 CCTACTCTCAGTGGCATTCTTGCCAAACGCAAGAGGATTATAGAGA 7929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 5798 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 05-JUN CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                             4.0%;
48.0%;
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                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                             Score 32.4; D. Pred. No. 2.5;
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US-08-796-101-39
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.0%; Score 32.4; DB 4; Length 5798; Best Local Similarity 48.0%; Pred. No. 2.5; Matches 122; Conservative 0; Mismatches 131; Indels 1.
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INFORMATION FOR SEQ ID NO: 33
SEQUENCE CHARACTERISTICS:
LENGTH: 5798 base pairs
TYPE: nucleic acid
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC COMPATIBLE
COMPUTER: PM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION US/08/796,101
FILING DATE: 05-FEB-197
CLASSIFICATION: 424
CONTROL OF THE PROPERTY OF THE PROPER
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ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE
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APPLICANT: PINCUS, STEVEN
TITLE OF INVENTION: RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,
TITLE OF INVENTION: PROPHYLAXIS AND THERAPY
NUMBER OF SEQUENCES: 184
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NAME: KOWALSKI, THOMAS J
REGISTRATION NUMBER: 32,
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2083 AAAGCTGTAGATTTTTCCAGAATGGATATTAAGGGAGATGATATTAGCAAAATGGGAATA 2142
                                                                                                                                                                   2024 TACCTACCAGTATCCCTATGAGATA-TTTTTTTAAACCGGTACTAAGAGAAAAAGTATCT 2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       608 ctgaagaaaccctgaacatagaggttgtaagatccaccatgcaggaggaggtggatgcag 667
                                                                           728 gtatcctggtatttttgagaaaaaaatctcaaggaaaaggcataaaaatgattgctaca 787
                                                                                                                                                                                                                                          668 cacagaccaaaactactgtgtgtgacttgttccgcaaccccagtatgcgtaaaaggatct 727
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SPEIR, EDITH
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RESULT 9
US-07-923-095-1
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TELEPAX: 203-321-2971
TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1730 base pairs
                                                                                                                                                                                                       Query Match 3.9%; Score 31.6; DB 1; Length 1730; Best Local Similarity 52.2%; Pred. No. 2.4; Matches 70; Conservative 0; Mismatches 64; Indels 0
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ATTORNEY/AGENT INFORMATION:
NAME: LOWNEY Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 06904-0060
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY:
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                                                                                                                                      1529 CCCTTTATGGTGGGCTTTGTTTGTTTTAAAGCCACGGACAATGGCACAGCTTACCTCAG 1588
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                                                               1589 TGGGAGATGCAAGATGAGTACCAGGGGGTGGTTAGGAATAATTTCTAAGTTTTTCCACCT 1648
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1649 TGAATGCTGAGTGG 1662
                                                                                                                                                          343 ccctgtgtggatgggtatatgatcaaagctacttcccttcgaccattgtgactaag 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Stamford
STATE: CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 19920
                463 ggaatgctggtggg 476
                                                                                                403 tgggacctggtatgtgattatcagtcactgaaatcagtggttcaattcctacttctgact 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
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US-08-314-979-1
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Sequence 1, Application US/08314979 Patent No. 5607843 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Ziai, I
                                                                                                                          1649 TGAATGCTGAGTGG 1662
                                                                                                                                                                                                                                                                 1529 CCCTTATGGTGGGCTTTGTTTGTTTTAAAGCCACGGACAATGGCACAGCTTACCTCAG 1588
                                                                                                                                                                                           1589 TGGGAGATGCAAGATGAGTACCAGGGGGTGGTTAGGAATAATTTCTAAGTTTTTCCACCT 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/922,307
FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,095
FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 617-861-6240
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                               463 ggaatgctggtggg 476
                                                                                                                                                                                                                       403 tgggacctggtatgtgattatcagtcactgaaatcagtggttcaattcctacttctgact 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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LENGTH: 1730 base pairs
                                                                                                                                                                                                                                                                                         343 ccctgtgtgggttgggttatatgatcaaagctacttcccttcgaccattgtgactaag 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
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ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
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TITLE OF INVENTION: Apamin Binding Protein/Receptor
NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Carroll, Alice 0.
Carroll, Alice 0.
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Sokol, Patricia Tyson
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US-08-436-716-1

Sequence 1, Application US/08436716 Patent No. 5652111 GENERAL INFORMATION:

APPLICANT:

Sokol Dr., Patricia T.

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; LOCATION:
US-08-314-979-1
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                                                                                                                                                                                  Matches
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TITLE OF INVENTION: Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 203-321-2971
TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO:
1649 TGAATGCTGAGTGG 1662
                                                                                                            1529 CCCTTTATGGTGGGCTTTGTTTGTTTTAAAGCCACGGACAATGGCACAGCTTACCTCAG 1588
                                                            1589
                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                       403 tgggacctggtatgtgattatcagtcactgaaatcagtggttcaattcctacttctgact 462
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                       463 ggaatgctggtggg 476
                                                                                                                                  343 ccctgtgtggatggctgggtatatgatcaaagctacttcccttcgaccattgtgactaag 402
                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1730 base pair
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lowney Dr., Karen REGISTRATION NUMBER: 312 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                 TGGGAGATGCAAGATGAGTACCAGGGGGTGGTTAGGAATAATTTCTAAGTTTTTCCACCT 1648
                                                                                                                                                                               70;
                                                                                                                                                                          h 3.9%; Sco
Similarity 52.2%; Pro-
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140..1456
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Ziai Dr., Mohammad R.
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                                                                                                                                                                          Score 31.6; DB 1; Length 1730; Pred. No. 2.4; 0; Mismatches 64; Indels 0
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RESULT 13
PCT-US92-06840-1/c
; Sequence 1, Application PC/TUS9206840
; GENERAL INFORMATION:
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Best Local Similarity
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TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1730 base pairs
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TITLE OF INVENTION:
tent No. 5652111
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CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2361
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                      1589 TGGGAGATGCAAGATGAGTACCAGGGGGTGGTTAGGAATAATTTCTAAGTTTTTCCACCT 1648
                                                                                                                                                     1649 TGAATGCTGAGTGG 1662
                                                                                                                                                                                                                                                                                           1529 CCCTTTATGGTGGGCTTTGTTTTTTAAAGCCACGGACAATGGCACAGCTTACCTCAG 1588
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              APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                              343 ccctgtgtggatggctgggtatatgatcaaagctacttcccttcgaccattgtgactaag 402
                                                                                                                                                                                  463 ggaatgctggtggg 476
                                                                                                                                                                                                                                                      403 tgggacctggtatgtgattatcagtcactgaaatcagtggttcaattcctacttctgact 462
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 140..1456
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1937 West Main Street
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            Shi, Yang
Seto, Edward
Shenk, Thomas
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                                                                                                                                                                                                                                                                                                                                                                 64; Indels
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Best Local Similarity
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TELEX: 236925
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2353 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: M-12594 CIP (1570-8)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/746,485
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Hom
                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                       2273 ACAACTGAGCACCACTTTCTGTAACTGAACAGGCAAAGAAATTACACTGAACATCAGCAT 2214
                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
2153 TTAAATCAC 2145
                                                                 2213 CTGGCAGTATTTTTTTGGAAAAAAAAAAGTGACTAAAATGGGTTTAAATTGATTAACACTA 2154
                                                                                     729 tatoctggtatttttgagaaaaaatctcaaggaaaaggcataaaaatgattgctacac 788
                                                                                                                                                                     669 acagaccaaaactactgtgtgtgacttgttccgcaaccccagtatgcgtaaaaggatctg 728
                               789 aaaagtgac 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2353 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL TYPE: tumor
                                                                                                                                                                                                                                                                                                                                                                            CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE: HeLa cells Carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY:
                                                                                                                                                                                                              68; Conservative
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1180 Avenue of the Americas - 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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52.7%;
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RESULT 14

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chen, Fang
TITLE OF INVENTION: DAM MOLECULES ENCODING HUMAN NUCLEAR
TITLE OF INVENTION: RECEPTOR PROTEINS
FILE REFERENCE: 19999Y
CURRENT APPLICATION NUMBER: US/09/141,000
CURRENT APPLICATION NUMBER: US/09/141,000
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTEQ for Windows Version 3.0
SOFTWARE: FASTEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 458
TYPE: PRT
ORGANISM: Human
US-09-141-000-4
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; SEQ ID NO 9

; LENGTH: 3741

; TYPE: DNA

; ORGANISM: H.sapiens

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; Sequence 4, Application US/09141000
; Patent No. 6054295
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APPLICANT: Nislow, Corey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Antifungal Assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
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264 TM.HSH.BA.H.KTR.M...TB..DSB.MNR.MMT..B...N.R.SN.TH.YYMRM.YCC 205
                           215 tettgagaatetetateeeactagaeteeaaatetgaggeeagagaagtgtegtegetttg 274
                                                                                         324 ..H..S.SYRBBC....KWTS...SK.HT.S.AS.C..DMTWC..BB..YHT.HG.AA. 265
                                                                                                                                      155 acatgctggacaataatactggatctggtaatgaaactggaatcctcagtgaagatgccc 214
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                                                                                                                                                                                                                                                                                                                                                                                 / Match 3.9%; Score 31; DB 3; Length 458; Local Similarity 9.2%; Pred. No. 1.8; Local Similarity 9.2%; Mismatches 205; Indels
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Search completed: July 1, 2002, 15:40:20 Job time: 10469 sec

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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                                                      BI102429
    BC016496
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                                                                    AQ280703 CITBI-E1-
AQ280703 CITBI-E1-
AQ280563 CITBI-E1-
AA682573 zj20a06.s
BG566618 602585464
BI338656 362506 MA
AQ237446 RPCIII-69
BG972774 602837672
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                                             AW107114 um18h07.y
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AI315917 uJ2/105.Y AW012307 um07c06.Y	u193a06.	ul75d06.y	BT308477 602985750	11n75f02.v	6021084	AW4/0401 M33407.V	un66c08.	BB637428	BF788430 602114177	BB661292 BB661292	AW475229 un63c01.y	AW259000 um76b08.y	BI143310 602907858	AA033971 z105c09.r	BB661317 BB661317	AT663462 uk33b05.y	BT332219 602981678	BT763962 603049842	AI316141 u125e04.y	AT746617 ul01d05.y	нв660738 вв660738	V60533	BB602405 BB602405	в66075	BB654082	മാ

ALIGNMENTS

LOCUS RESULT AV652088 COMMENT REFERENCE KEYWORDS VERSION ACCESSION FEATURES AUTHORS ORGANISM JOURNAL TITLE source Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z. Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver with those of corresponding noncancerous liver with Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001) AV652088 615 bp mRNA linear EST 15-JAN-2002 AV652088 GLC Homo sapiens cDNA clone GLCCWF10 3', mRNA sequence. AV652088 Contact: Zeguang Han Chinese National Human Genome Center at Shanghai Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China 1918 B6-21-50801919 (ex.45) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens AV652088.1 GI:9873102 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai. 21625106 human. Fax: 86-21-50801922 (bases 1 to 615) /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI" /tissue_type="corresponding non cancerous liver tissue" /dev_stage="Adult" /lab_host="SOLR" 1. .615 /organism="Homo sapiens" /db_xref="taxon:9606" Location/Qualifiers /clone_lib="GLC" /clone="GLCCWF10"

BASE COUNT

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RESULT 2
AV699858/c
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ORGANISM
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                                                                                                                                                                                                                                                                                                                        607 GTGGCCAT 614
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Local Similarity 91.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCATTCCTGGTCATCGTTGCTGGGTCCACATGCTGGACAATAATACTGGATCTGGTAATG
                    Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
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                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 779)
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                                                                                                                                               Homo sapiens
                                                                                                                                                                                                               AV699858 GKC Homo sapiens cDNA clone GKCDLE04 3', mRNA sequence.
                                                                                                                                                                                           AV699858.1 GI:10301829
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1630 gcaaaggccaggttcagcaattttcaaactgtatgtacatttaataaaataactataaat 1689
                                                  1570 attttaaacaaatagctggtatagtttacaatattataaagatattgttcaaattgaagg 1629
                                                                                            1450 aaagattagatactaaataacattgactatctcttttgtaaatacagtcactaaatgatgt 1509
                                                                                                                                                                                                                                         1390 gacctatataaatgcatttaatacatgatacttttgacataataagccattggaaaacgg 1449
                                170 ATTTTAAACAAATAGCTGGTATAGTTTCCAATATTATAAAGATATTGTTCAAATTGAAGG 111
                                                                                                                                                                                                                                                                                                     1270 tcacagaattaggatgtggctggctggtgtatgaagcaccatgtgatgaattcataaagt 1329
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                                                                                                                                                                                                                         GACCTATATAAATGCATTTAATACATGATACTTTTGACATAATAAGCCATTGGAAAACGG
                                                                                                                                                                                                                                                                                                                                                   TCCCAGAATTAGGATGTGGCTGGCTGGTGTATGAAGCACCATGTGATGAATTCATAAAGT 411
                                                                                                                                                                                                                                                                                                                                                                                                              AAAGTTCCAAATTTATCCATAATTTCTAGTAGATTAAGATGATTCAGAACCAAAAGAAAA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: hanzg@chgc.sh.cn
This clone is available at CHGC in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, 201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zeguang Han
Chinese National Hum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="GKCDLE04"
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                                                                                                                                   177 ttcacaatcaatggcctttgaggagctcttgagtcaagttggaggccttgggagatttca 236
                                                         357
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                                                                                                                                                                                                                                                                                                                 Local Similarity
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tactggatctggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctat 416
                                                                                            agagaactttgctgcagccattcctggtcatcgttgctgggtccacatgctggacaataa 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jpp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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troglodytes male_lymphoblast DNA, clone_lib:PTB Chimpanzee Male
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
/clone_150 c 154 g 207 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="PTB-106L08.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pan troglodytes"
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Pred. No. 4.3e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 GGATGGCTGGGTATATGATCAAAGCTACTTCCCTTCGACCATTGTGACTAAG 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA680184 399 bp mRNA linear EST 19-DEC: zillc10.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:430482 3' similar to TR:G1293672 G1293672 G1293672 FIDERY SPECIFIC TRANSPORT PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptce,M., Tan,F., Theising,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA680184.1 GI:2656651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             White,Y., Wylie,T., Waterston,R. and Wilson,R. washU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 399)
                                                                                                                       constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:430482"
 22.7%;
99.7%;
Score 387; DB 9; Length 399; Pred, No. 7.3e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        809 acatagaggttgtaagatccaccatgcaggaggagctggatgcagcacagaccaaaacta 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 TAAAGGCACTTAGAAAAGTTGCACGCACAAATGGAATAAAGAATGCTGAAGAAACCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                749 taaaggcacttagaaaagttgcacgcacaaatggaataaagaatgctgaagaaaccctga 808
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                                                                                                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://ork.page.
                                                                                                                                                                                                                                                                                                                              Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                               Seq primer: M13 Reverse Class: BAC ends.
                                                                                                                                                                                                                                               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_GSSs: CITBI-E1-2514B2.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 612)
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CITBI-E1-2514B2.TR CITBI-E1 Homo sapiens genomic clone 2514B2, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ280703.1 GI:3906522
  /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: ECORI; Site_2: ECORI;
CalTech Human BAC Library D"
a 80 c 101 g 189 t
                                                                                    /clone_lib="CITBI-E1"
/sex="male"
                                                                                                                           /db_xref="taxon:9606"
/clone="251482"
                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                     High quality sequence stop: 474.
                                                                                                                                                                        Class: BAC ends
                                                                                                                                                                                                      Sequence Tagged Connector
                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
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                                                                                                                                                                                                                                                                                                                                                                                       scanning the
                                                                                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                         Mahairas, G.G., Waliace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EuRaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 474)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
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Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                         jwallace@u.washington.edu
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                                                                                                                                                                                            3091
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                            /clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                          /clone="Plate=3091 Col=4 Row=D"
                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                    Location/Qualifiers
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                      source
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CITBI-E1-2514B1.TR CITBI-E1 Homo sapiens genomic clone 2514B1, DNA
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                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 578)
                                                                                                                                                                                                                                                                         Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                             Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                              Use of a random human BAC End Sequence Database for Sequence-Ready
                                                    Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                        Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                              9712 Medical Center Dr., Rockville, MD 20850, USA
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                                                                             http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 AAATAACTATAAATTAAAAATTATATTTC 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATTGGAAAACGGAAAGATTAGATAACTAAATAACATTGACTATGTCTTTGTAAATACAGG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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2j20a06.sl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA
clone IMAGE:450802 3' similar to TR:G1293672 G1293672
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases I to 367).

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Hillier,L., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin Krizman,D., Kucaba,T., Cacy,M., Le,N., Lennon,G., Marra,M., Martin Krizman,D., Kucaba,T., Kucaba,T., Steptoe,M., Tan,F., Theising,B., J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., J., Moore,B., Walte,T., Waterston,R. and Wilson,R. White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIDNEY-SPECIFIC TRANSPORT PROTEIN. ;, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      AA682573.1 GI:2669854
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                        Unpublished (1997)
Contact: Wilson RK
                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
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a 79 c 88 g 182 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="2514B1"
/clone_lib="CITBI-E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="sperm"
/note="Vector: pBel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 AGAATGCTGAAGAAACCCTGAACATAGAGGTTGTAAGATCCACCATGCAGGAGGAGCTGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 TCATAGTTGCCCATGTCTCAGACAGTTGGCTGGTGGAATCTGCTCGGTGGTTGATAATCA 304
                                                                                                                                                                                                                                                                                                                   3 AGA 1
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             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 754)
                                                                                                                     Homo sapiens
                                                                                                                                                                                            602585464F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4714598 5
                                                                                                                                                               BG566618.1 GI:13574271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="20 week-post conception fetus"
/lab_host="DHIOB (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT/T3D (Pharmacia)
with a modified polylinker; Site_1: Pac ; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:450802"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 4.5e-48;
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567 CACCTGAATGGGACCTTCCCCCAACACAAGTGACGCAGACATGGAGCCCCTGTGTGGAATGG
                                                                                  484 cacctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtgg-atgg 542
                                                                                                                             507 GACTCAAACATGAGGCCAGAGAAGTGTCGTCGCTTTGTTCATCCTCAGTGGCAGCTCCTT 566
                                                                                                                                               424 gactcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttctt 483
                                                                                                                                                                                              447 TCTGACAATGACACTGGGGCCCTCAGCCAAGATGCACTCTTGAGAATCTCCATCCCACTG 506
                                                                                                                                                                                                                364 totggtaatgaaactggaatcotcagtgaagatgcoctottgagaatototatocoacta 423
                                                                                                                                                                                                                                                             387 TTCACTGCATTCATACCTGCCATCGCTGCGTGCACACACCTGGACAATGACACTGTC 446
                                                                                                                                                                                                                                                                                304 tttgctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactgga 363
                                                                                                                                                                                                                                                                                                                          327 CAGACTGTTTTTCTCTCAATCTTTGCTGTTGCTACATACCTTCATTTTATGCTGGAGAAC 386
                                                                                                                                                                                                                                                                                                                                                          244 catctggttttttattcttccctctctcatgttattaatccctcatatactgctagagaac 303
                                                                                                                                                                                                                                                                                                                                                                                                              184 tcaatggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgctt 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 CTCTTTGAACCTCTCTGGATACAGTCATTTTGCCTCTACTTGAGGATCAACTGTTCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 agaaattgatgcgaggatcaatacaagcttaatttgaattaataaaaggaaatattttct 123
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                                                                                                                                                                                                                                                                                                                                                                                           TCAATGGCCTTTCAGGACCTCCTGGGTCACGCTGGTGACCTGTGGAGATTCCAGATCCTT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence
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/Clone_lib="NHI_MGC_T/6"
/Clone_"Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (9gccgccteggco;); Site_2: Sfil (9gccattatggco;); and
sequence: 5'-CACGGCCATTATGCCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGAGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
by CR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                        111 ggaaatattttctccctttgaacttatctccgtaaagccattgtgcctcctcttgggggt 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                   171 cacgtgttcacaatcaatggcctttgaggagctcttgagtcaagttggaggccttgggag 230
291 actgctagagaactttgctgcagccattcctggtcatcgttgctgggtccacatgctgga 350
                                                                                       231 atttcagatgcttcatctggtttttattcttccctctctcatgttattaatccctcatat 290
                                                                                                                               57 CACCTGTTCA----CAATGGCTTTTGAGGAGCTCCTGAATGAAGTCGGTGGCTTGGGGAA 112
                                                                                                                                                                                                        1 GAAAACTTTTTCTCCCTTTGA----CTTACTTATAAATCCATGTGACTCCTCTTGAGGAC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       581 bp mRNA linear 362506 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence. BI338656
                                                       BI338656.1 GI:15031939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fahrenkrug, S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 131 row: H column: 23 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."

163 c 136 g 159 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                    19.3%; Score 328.8; DB 10; Length 75.2%; Pred. No. 3.1e-45; ative 0; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
                                                                                                                                                                                                                                                                                                                              Length 581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   591 ggacctggtatgtgattatcagtcactgaaatcagtggttcaattcctacttctgactgg 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 741)

1 (bases 1 to 741)

1 Adams, M. D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                 Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0208

Email: mdadams@figr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the contact pleter de Jong

library availability, please contact pleter de Jong

(pleter@dejong.med.buffalo.edu). Clones may be purchased from

Rejecter@dejong.med.buffalo.edu). BAC end search page:

Research Genetics (info@resgen.com). BAC end search page:

Research Genetics (info@resgen.com). BAC end search/bac_end_search.html

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mark Adams
                                                                                                                                                                                                                                                                                               Class: BAC ends
                                                                                                                                                                                                                                                                                                                    primer: T
                       /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                       /db_xref="taxon:9606"
/clone="RPCI-11-69K14"
/clone_lib="RPCI-11"
                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:7526365"
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                               /sex="Male"
       156 c
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                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
http://image.llnl.gov
Plate: LLAM10958 row: o column: 18
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                        High quality sequence start: 13 High quality sequence stop: 819
                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 820)
                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602837672F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4972265
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                                                                                                                                                                                                                                                                                                                                                                                                           640 cttctgactggaatgctgggtgggaggcatcataggtgggccatgtctcagacaggt 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 572 GTGACTGAGTGGGACCTGGTGTGTGAATCTCAGGCACTGAATTCTGTTGCTAAATTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580 gtgactaagtgggacctggtatgtgattatcagtcactgaaatcagtggttcaattccta 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       520 gacacagaaccctgtgtggatggctgggttatatgatcaaagctacttcccttcgaccatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 ACCTAGGAAGATTCCAGATCCTTCAGATCTCTTTTGTTCTCTTCCTCGTAGGCCTTGTG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 ggccttgggagatttcagatgcttcatctggttttttattcttccctctccatgttatta 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 CCCATCGGAGATAGTCATTCAGTTCCAATGGCCTTTCAGGAACTCCTGAATCAAGTTGGA 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCCAACCACAGTGGCATCTTCTTCATTTGAATGGCACTTTCTCCAATGAGACAGAGCCA 511
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 866)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC) Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                           Mus musculus
                                                                                                                                                                                                           EST
                                                                                                                                                                                                                        BI102429.1 GI:14553322
                                                                                                                                                                                                                                                                     BI102429
602889616F1 NCI_CGAP_Kidl4 Mus musculus cDNA clone IMAGE:5044850
5', mRNA seguence
                                                                                                                                                                                    house mouse.
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    mRNA sequence.

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/clone=lib="NCI_CGAP_Kid14"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (TI phage=resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SaI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. | "
a 197 c 185 g 247 t
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/strain="FVB/N"
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Pred. No. 3.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCCTAGGAAGATTCCAGATCCTTCAGATCTCTTTTGTTCTCTTCCTCGTAGGCCTTGTG
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                                                                                                                                                                                                                                                                        cttctgactggaatgctggtgggaggcatcataggtggccatgtctcagacaggtgg 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gacacagaaccctgtgtggatggctgggtatatgatcaaagctacttcccttcgaccatt 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACACTGAGCCCTGTGTGGATGGTTTGGGTGTATGACAGGAGCAACTTCCTTTCTACCATT 565
                                                                                                                                                                                                                                              ATTCATGATTGGCTATTTATAGGGGCTATCATATGTGGCCATTTGTCAGACAGGTTG 682
                                                                                                                                                                                                                                                                                                                                                   GTGACTGAGTGGGACCTGGTGTGTGAATCTCAGGCACTGAATTCTGTTGCTAAAATTTTC 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop:
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Plate: LLAM11122 row: p column: 03
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                                            AW107114 739 bp mRNA linear Lot 40 001 mm18h07.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2192701 5' similar to TR:070609 070609 PUTATIVE INTEGRAL
AW107114
                            MEMBRANE TRANSPORT PROTEIN. ;, mRNA sequence.
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
a 206 c 189 g 268 t 1 others
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/strain="FVB/N"
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/clone="IMAGE:5044850"
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71.7%;
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pred. No. 1.8e-39;
0; Mismatches 152;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                           160 ctcttgggggtcacgtgttcacaatcaatggcctttgaggagctcttgagtcaagttgga 219
                                    380 CCCATCCTTGACAATGACACTGCCTCTGATAATGGCAGTAGGATACTGAGCCAAGATGAC
                                                                340 cacatgctggacaataatactggatctggtaatgaaactggaatcctcagtgaagatgcc 399
                                                                                                                                            320 GTACCACATATTGGAATGGAGAACTTTACTGCAGCCATTCCCAATCATCGCTGCTGGGTC
                                                                                                                                                                                                                                                                                                 220 ggccttgggagatttcagatgcttcatctggtttttattcttccctctctcatgttatta 279
                                                                                                                                                                                                                                                                                                                                                            200 CCCTTTGGAAATAGTTATTCAACCTCAATGTCCTTTCAAGAACTCCTGAATCAAGTTGGA 259
                                                                                                                                                                     atcoctcatatactgctagagaactttgctgcagccattcctggtcatcgttgctgggtc 339
                                                                                                                                                                                                                                                    AGCCTAGGAAGATTCCAGATCCTTCAGATAGTTTTTCTTTTCCTCCTCAATGCCATTGTA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382;
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The WashU-NCI Mouse EST Project 1999

The WashU-NCI Mouse EST Project 1999
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 314 286 1810
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Washington University School of Medicine
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for
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/clone="IMAGE:2192701"
/clone_lib="Sugano mouse kidney mkia"
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                                       TGGCCTTTCAGGAACTCCTGAATCAAGTTGGAAGCCTAGGAAGATTCCAGATCCTTCAGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9848 row: d column: 18 High quality sequence stop: 665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be
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Site_2: Sall; Cloned unidirectionally. primer: Oli.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
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Search completed: July 1, 2002, 14:44:55 Job time: 9394 sec

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1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
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Listing first 45 summaries
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ion US/0917; Mary Jane Gary B. Goott R. JOHITORING J MONITORING J MONI		03 448 3 3 4 4 4 8 8 3 3 4 4 4 8 8 3 3 4 4 4 8 8 3 3 4 4 8 8 3 3 4 4 8 8 3 4 8 8 8 3 4 4 8 8 3 4 8 8 8 8	
Jane Jane Frey J. FRING TOX1 10-13 10-13 7713H1	.	- SD - SD - SD - SD - SD - SD - SD - SD	
9172711 ane ane y J. NG TOXICOLOGI NG TOXICOLOGI 195/09/172,711 -13 8; Score 98.4 8; Score 98.4 8; Pred. No. 0; Mismata accatt gtgcc acttattattgt trigagccaagttg ctgaatcaggtag tctctcatggtag tctctctatgttattg ccatcgttgctggg ccatcgttgctggg	ALIGNMENTS	08-998- 08-998- 08-998- 08-451- 08-319- 08-998- 09-056- 09-056- 09-071- 08-323- 08-954- 08-954- 08-329- 09-390- 08-526- 08-526- 08-526- 09-031-	
72711 3 TOXICOLOGICAL RES TOXICOLOGICAL RES (09/172,711 3 Score 98.8; DB 4 Pred. No. 2.9e-16 (0; Mismatches (0; Mismatches (1	ENTS	98-416-1036 998-416-538 998-416-538 3-98-416-058 3-11-4058-2 3-11-704-5 3-162-632-4 3-98-416-288 3-998-416-288 3-998-416-19-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-119-15 3-007-107-107-107-107-107-107-107-107-107	
RESPONSES DB 4; Lengtl pb 1; Inde: \$ 67; Inde: \$ (67); Inde: \$ (11)		11	
NNSES Length Length ; Indel ; Indel ; gagatatt gagagattt			
OGICAL RESPONSES 711 711 8.8; DB 4; Length 280; No. 2.9e-16; Indels 2; Carlothes 67; Indels 2; Carlothes 67; Indels 1		sequence	
ch 280; ls 2; Ga lill			,
Gaps at 184 l tc 244 tc 244 tc 168 cct 304		538, App 305, App 305, App 4, Appli 5, Appli 6, Appli 1, Appli 2, Appli 2, Appli 2, Appli 1, Appli	,
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RESULT 2
US-08-232-463-14/c
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:

APPLICANT:

DORNER, F. SCHEIFLINGER, F.

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US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
INFORMATION FOR SEQ ID NO:
                                                                                                                       952 aggcataaaaatgattgctacacaaaagtgaccaaattttaagaagccttcatgagctga 1011
                                                                                       772 cgcacaaatggaataaagaatgctgaagaaaccctgaacatagaggttgtaagatccacc 831
                                                                                                                                                                                                                                                                              712 cggtggttgataatcaccaataaactagatgagggcttaaaggcacttagaaaagttgca 771
                                                                                                                                                                                                                                                                                                                                           652 atgctggtgggaggcatcataggtggccatgtctcagacaggtggctggtggaatctgct 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                           y Match
Local Similarity 8.7%; Score 60.4; DB 1; Length 7218;
Local Similarity 8.7%; Pred. No. 6.5e-06;
hes 40; Conservative 228; Mismatches 194; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/232,463 FILING DATE:
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US-07-867-106-2
                       Query Match 3.2%;
Best Local Similarity 49.1%;
             Matches 173;
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Patent No. 5389526
                                                                                                                                           FEATURE:
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                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US
FILING DATE: 19920625
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1049 CCTGCAGCCAAGCTCGGAATTAATTCTGTGAGCGTATGGCAA 1008
                                                                                                           LOCATION:
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                                                                                                                                                                        NAME/KEY:
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COUNTRY: ULL
19103
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REGISTRATION NUMBER: 35,13
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APPLICATION NUMBER: PCT/AU90/00530
                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                NAME:
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          Conservative
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                                                                                                                                                                                                                                                single
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                Score 54; DB 1; Length 5852; Pred. No. 0.00025;
Mismatches 175; Indels
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                                                                                   US-08-647-397-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1585 ctggtatagtttacaatattataaagatattgttcaaattgaagggcaagggccaggttc 1644
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Beier, David R. APPLICANT: Brady, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2102 base pairs
                                                                                                                                   FEATURE:
                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 600 A
                                                                                                                                                                                ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DUS/MS-LV-
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                         STRANDEDNESS: double
                                                                                                                                                ORGANISM:
                                                                                                     LOCATION:
                                                                                                                    NAME/KEY:
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600 Atlantic Avenue
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08487826B Patent No. 5993827
                                                                                                                             ; ANTI-SENSE: US-08-487-826B-13
GENERAL INFORMATION:
                                                       Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                           TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 TGCATCTGCCAAACGCCAGTCTTCCCAATGACACCCAGGGGGCCACCGAGCCATGCTTGG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 ttcttcacctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtgg 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Su, Xin-zhaun APPLICANT: Wellems, Thoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                              HYPOTHET ICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 620 Newport Center Drive CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                   NAME:
                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chitnis, Chetan
Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peterson, David S.
                                                                                                                                                NO
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                                                                                                                                                                                            linear
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                                                                                                                                                                                CDNA
                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                               235-8550
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                                                                           2.9%; Score 49.6; DB 2
43.8%; Pred. No. 0.0054;
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                                                                                                                                                                                                                                                                                                                                                                                                             US/08/487,826B
                                                                                                                                                                                                                                                                                                                                       29,655
                                                                                                                                                                                                                                                                                                                            NIH121.001CP1
                                                              0; Mismatches 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16th Floor
                                                                                            DB 2; Length 19124;
                                                                      Indels
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US-08-731-722-5

; Sequence 5, Applic
; Patent No. 5961971
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                                                                           TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Martin
     MOLECULE TYPE:
                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1186 base pair
                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 352-375-8100
                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Whitlock, Ted W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15961 AAAATTAATTACATGC 15976
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Biocont.
TITLE OF INVENTION: by Pyth.
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                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1441 ggaaaacggaaagattagatactaaataacattgactatctctttgtaaatacagtcact 1500
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                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1261 aaaagaaaatcacagaattaggatgtggctggctggtgtatgaagcaccatgtgatgaat 1320
                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                              CLASSIFICATION:
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                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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STREET: 2421 N.W. 41st Street, Suite A-1
                                        nucleic acid
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                 linear
DNA (genomic)
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by Pythium oligandrum
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US-08-998-416-541/c
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                                                                                                                                                                                                                                                   Sequence 541, Application US/08998416 Patent No. 6239264 GENERAL INFORMATION:
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                                                    APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
COMMBER OF SEQUENCES: 1152
ADDRESSER: NO CRESS:
ADDRESSER: NO CRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 45.78;
Matches 290; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                             1664 gtacatttaataaaattaactataaaattaaaaaat 1697
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                                                                                                                                                                                                                                                                                                                                                                          750 ATATCTTTAAAAAGATATAAATTAATTACATAAT 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             638 TCTATTTTAATAAATAATCGTAATACTTTAATAAGAAATA-----AATAATTAATAT 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1364 gaaatcaaaataaatccagaaatagagacctatataaatgcatttaatacatgatacttt 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1304 agcaccatgtgatgaattcataaagttgcaaaagtcaaaacaatactgtacatgcaacca 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   578 ATAAGAAATTCTTCAATAGAGAAAGGTTTTATTTTTCAATAGAAAATTGTAATTCTTAT 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 ATATTTTAAATAATGATCTGGATTTATACAGTAGATCCTATAAATCTTTAATAGTAGTT 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 AAAATGAAAATACTTCTAATAAGAATATATTTATTATAAATATTGAAAAACTTTTATTT 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 AGCAATAGATTCAGTTAAAGCGAAACCTAAAATAGCTGTTCTTGTTAAATCTTGTTGTAA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 TTTTATTAACTTAAATTAAAAAGCGAATAAAATTAAGAAAGCAATCATTAAACAGAATAA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: 23-5
: 3054 Cornwallis Road
Research Triangle Park
                                                                                                                                       Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                Mohr, Christine
                                                                                                                                                                                               Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                  Philippsen, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Pred. No. 0.0027;
0; Mismatches 332; Indels 12
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Tue Jul

COUNTRY: STATE:

USA

27709

CLASSIFICATION: APPLICATION NUMBER: FILING DATE:

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Query Match 2.8%; Score 47.8; DB 4; Length 821; Best Local Similarity 47.7%; Pred. No. 0.0042; Indels Matches 124; Conservative 0; Mismatches 136; Indels
                                                      Sequence 36, Application US/08883795A

Sequence 36, Application US/08883795A

Sequence 36, Application US/08883795A

Sequence 36, Application US/08883795A

Patent No. 5985607

APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor

APPLICANT: Awang, Gregor

TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
TITLE OF INVENTION: Vectors 39

NUMBER OF SEQUENCES: 39

NUMBER OF SEQUENCES: 39
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Relactions of the Potentin Relaction 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1445 aacggaaagattagatactaaataacattgactatctctttgtaaatacagtcactaaat 1504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         732 AAGGGTAANTNTAAATGCAAATTATTATTAGGGGTCGTTTTNTCATTTTTTTATTATTATTA
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                                      CORRESPONDENCE ADDRESS:
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31-DEC-1996
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E: BERESKIN & PARR
40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
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; CLONE: Rh 32
US-08-883-795A-36
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 50.0 Matches 170; Conservative
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                                                                                                                                                                                                                                           US-08-451-405A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DM PC COMPATIBLE
COMPANING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                          sequence 2, Application US/08451405A
Patent No. 5736358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1367 atcaaaataaatccagaaatagagacctatataaatgcatttaatacatgatacttttga 1426
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FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,2
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                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1605 ataaagatattgttcaaattgaagggcaaaggccaggttcagcaattttcaaactgtatg 1664
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APPLICANT: FASEL, CHRISTOPHE DOMINIQUE
APPLICANT: REYMOND, CHRISTOPHE DOMINIQUE
TITLE OF INVENTION: DICTYOSTELID EXPRESSING A DESIRED PROTEIN
TITLE OF INVENTION: METHOD FOR EXPRESSING A DESIRED PROTEIN
NUMBER OF SEQUENCES: 3
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                               266 ATAATTAAAATGTTTATAATTAA----ATATTTTATAATTAAAATGTTTATAATTACATA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 TITTATAAATAATTAAAATTACATATTTATAATT 361
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US-08-998-416-541

ORGANISM

MOLECULE TYPE: ORIGINAL SOURCE:

TOPOLOGY: STRANDEDNESS:

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ADDRESSEE:

Toronto

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RESULT 10
US-07-867-106-2/c
Patent No. 535322.

GENERAL INFORMATION:
GENERAL IN
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,273
PRILING DATE: 15-JAN-1993
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 731
                                                                                                                                                                                                                                                                                                                                                                                                                                          1533 tttaattacttttctttgtaatttttctct 1563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1353 acatgcaaccagaaatcaaaatccagaaatagagacctatataatgcatttaata 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK
COMPUTER: Midwest Micro 486-50
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
PILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1293 ctggtgtatgaagcaccatgtgatgaattcataaagttgcaaaagtcaaaacaatactgt 1352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 TTTTTCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAATAAATTAGAATAAAAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ATTTTTGTGTTCTTATAATTTGGTTAAATCGATGAATAATATTTGATTAGTATATGTTTT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
Local Similarity 43.7%; Pred. No. 0.026;
ses 197; Conservative 0; Mismatches 254; Indels 0; Gaps
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; NAME/KEY: CDS; LOCATION: 2378..5038
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1492 acagtcactaaa--tgatgttagttacttttccatggtggaattttaattactttttctt 1549
                                                  1432 taagccattggaaaacggaaagattagatactaaataacattgactatctctttgtaaat 1491
                                                                                                    2199 AATAAATATAATTAAAATTGTCATGCCAAAACTGATAAATATTTGATATATTATCCAATA 2140
                                                                                                                     1312 gtgatgaattcataaagttgcaaaagtcaaaaacaatactgtacatgcaaccagaaatcaa 1371
                                                                                                                                                                                                                        1192 ttttgggaagtcctttaaaaagttacaaatttatcaataaattactagtagataagatga 1251
                                                                                                                                                                                                      TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA: APPLICATION UNMBER: AU BJ 7187
APPLICATION NUMBER: PCT/AU90/00530
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Une L. CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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2378..5038
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1550 tgtaatttttctctctgtatatttttaaacaaata 1583

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RESULT 11
US-08-883-795A-36/c
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Best Local Similarity 47.9%;
Matches 186; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Delcuve, Genevapplicant: Awang, Gregor TITLE OF INVENTION: Recon
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08, FILING DATE: 27-JUN-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Gravelle, Micheline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                              1315 atgaattcataaagttgcaaaagtcaaaacaatactgtacatgcaaccagaaatcaaaat 1374
                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: Rh 32
                                                                                                                                                                                                          1375 aaatccagaaatagagacctatataaatgcatttaatacatgatacttttgacataata- 1433
1554 attittetetetgtatattttaaacaaatagetggtatagtttacaatattataaagata 1613
                                                                                                                                      1434 agccattggaaaacggaaagattagatactaaataacattgactatctctttgtaaatac 1493
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COMPUTER: II
                                                                  1494 agtcactaaatgatgttagttacttttccatggtggaattttaattactttttctttgta 1553
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                                                                                                                                                                                                                                             410 ATGTAATTATAAACATTTTAATTATAAAAATATGTAATTATAAACATTTTAATTATAAAAT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gravelle, MICHELLIC REGISTRATION NUMBER: 40,261
                                                                                                                                                                         350 ATGTAATTATAAACATTTTAATTATAAAATATGTAATTATAAACATTTTAATTATAAAAT 291
                                   230 ATTTAATTATAAATATT--TTAATTATAAAATATTTAATTATAAATATTTTAATTATAAA 173
                                                                                                       TELEPHONE:
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Vectors for Tissue Plasminogen Activator
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APPLICANT: Moyer, F
APPLICANT: Hall, Ri
APPLICANT: Gruidl,
US-07-991-867B-8
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ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: UF TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
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                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          FEATURE:
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                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19-FEB-1991
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                             complement (234..782)
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Patent No. 5721352
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                        APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
CORRESPONDENCE ADDRESS:
ADDRESSE, Date 12.5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1412 ААААТТТССАЛАААСТАТАА 1431
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                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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             SOFTWARE:
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                                                                                                     COUNTRY: U
ZIP: 32606
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                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
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Local Similarity 45.5%; Score 43.6; DB 1; Length 1511;
Local Similarity 45.5%; Pred. No. 0.063;
nes 282; Conservative 0; Mismatches 324; Indels 14; Gaps
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                                                                                                                                        Florida
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PatentIn Release #1.0, Version #1.25
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Best Local Similarity
1232 AAAAAATTAATAATATCTAAAAATAAATTTGGTAACTTTAATAATGTTTTTCCTATTAG 1291
                 1496 tcactaaatgatgttagttacttttccatggtggaattttaattactttttctttgtaat 1555
                                                               1176 AATTGTGAATCATGTAATATAAATGACTATA----ATTTTATTAATAATTTAGTAAATTT 1231
                                                                                             1436 ccattggaaaacggaaagattagatactaaataacattgactatctctttgtaaatacag 1495
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INFORMATION FOR SEQ ID NO:
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NAME/KEY:
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ORIGINAL SOURCE:
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LENGTH: 1511 base pairs
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REFERENCE/DOCKET NUMBER: UF114.C2
TELECOMMUNICATION INFORMATION:
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FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
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45.5%; Pred. No. 0.063;
ative 0; Mismatches 324; Indels 14; Gaps
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                                                                                                                                           INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
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                   FEATURE
                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0:
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
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FILING DATE: 30-JAN-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1616 gttcaaattgaagggcaaag-gccaggttcagcaattttcaaactgtatgtacatttaat 1674
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NAME/KEY: CDS
                         ORGANISM: Amsacta moorei entemopoxvirus
                                                                                                        STRANDEDNESS:
                                                                                     TOPOLOGY:
                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: UE:
                                                                                                                                                                                                                                                                    NAME: Bencen, Gerard H. REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 01
FILING DATE: 19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/991,867 FILING DATE: 07-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                    nucleic acid
EDNESS: double
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                                                                DNA (genomic)
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US-08-998-416-1137/c

Sequence 1137, Application US/08998416 Patent No. 6239264

GENERAL INFORMATION:

APPLICANT: Rebischung, Corinne TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII TITLE OF INVENTION: AND USES THEREOF

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Wendland, Jurgen Knechtle, Philipp Pohlmann, Rainer Steiner, Sabine Mohr, Christine Philippsen, Peter

APPLICANT:

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1412 AAAATTTCCAAAAAGTATAA 1431
                                    1675 aaaataactataaattaaaa 1694
                                                                     1616 gttcaaattgaagggcaaag-gccaggttcagcaattttcaaactgtatgtacatttaat 1674
                                                                                                                                               1292 TATAGTTGAGTTAAATATGGAATCAATACAAATAAAAGATTATAAAATTTATAGAAAAATT 1351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/998,41
FILING DATE: 24 DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 919-541-8689
INFORMATION FOR SEO ID NO: 1137:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (96 ORIGINAL SOURCE: ORGANISM: PAG1692RP
                                                                                                                                                                                                                                                                                                                                                                                                                                               1260 caaaagaaaatcacagaattaggatgtggctggctggtgtatgaagcaccatgtgatgaa 1319
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CITY: Research Triangle Park
STATE: No. 6239264th Carolina
1560 ctctctgtatattttaaacaaatagctggtatagtttacaatattataaagatattgttc 1619
                                                                                                                                                           485 ATTAAAGTTAAAATTAATTTAATAATAATAATTCTTATAAAAAGATTAAATAATAATAAATCA 426
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ZIP: 27709
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                                                   246 TAATAACTAATTTAAAATTTGAACATAGACTAAATAGTATTCATATTAAATATTTTT 187
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Search completed: July 1, 2002, 15:40:48 Job time: 10497 sec

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Maximum DB seq length: 200000000
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Maximum Match 10
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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N_GENESEq_038002: *

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Listing first 45 summaries
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AAH98847
AAZ38316
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AAK70136
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AAK70137
    AAF55043
ABA08976
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            Human secreted pro
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                                    Nucleotide sequenc
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		-			e protein HPO2000"		<pre>sion; homology; nntibody; assay reagent; gene therapy;</pre>	0.					cDNA encoding a hu hoard DNA. Homo s Human polynuclecti Human protein havi Human protein havi Human transporter Human transporter Human organic anio Human foetal liver probe #8860 for ge Human bone marrow probe #11877 used Human reproductive Human reproductive Human foetal liver probe #11877 used Human reproductive Human foetal liver probe #17241 for g Human bone marrow probe #17241 for g probe #24865 used Rat EST-derived co Human cDNA 5'-end Human full-length Rat liver toxicolo Human full-length Rat liver toxicolo Human polynucleoti Human polynucleoti Human polynucleoti Human organic anio hoarl DNA. Homo s Human organic anio hoarl DNA. Homo s Human organic anio Mouse organic anio	Human polynucleoti

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             excretion, and may have a similar function. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these potentially useful therapeutically.
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tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human EST-derived coding sequence SEQ ID NO: 704
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200154477-A2
                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA biodiversity and for nutritional purposes.
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                                                                                                                                                                                                                                                                                                                                                                                                                      isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use \mbox{\ensuremath{^{-}}}
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AAZ38316

AAZ38316 standard; cDNA; 804 BP

AAZ38316;

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09-FEB-2000 (first entry)

HP02000; transmembrane domain; liver; expression; homology; Human transmembrane protein cDNA clone HP02000 coding sequence.

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                                        1027 caga 1030
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This sequence represents the coding sequence of human cDNA clone CC HP02000 which encodes a 32 kD protein with two putative transmembrane CC domains. The cDNA was isolated from a human liver cell cDNA library, and the common tissue localisation studies has been found to be expressed only in CC transporter (EMBL Accession No. Y0945) which is involved in drug CC transporter (EMBL Accession No. Y0945) which is involved in drug CC may be used to raise specific antibodies, as assay reagents, as CC diagnostic tissue markers, for the isolation of cognate receptors, CC ligands and binding proteins, and as biologically active agents. CC Nucleotides encoding the protein may be used as primers and probes or CC antisense molecules, and in gene therapy. Cells transformed with these CC potentially useful therapeutically.
                                                                                                                                                                                                                                                                                                                                   Matches
427 tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac
                                                      181
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                                                                                                                          121
                                                                                                                                                                                                                                                           187 atggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcat 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human proteins with transmembrane domains, involved in control of cell proliferation and differentiation, useful for treating e.g. cancer or
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P-PSDB; AAY52386.
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                                  ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
                                                    99taatgaaactggaatcctcagtgaagatgccctcttgagaatctctatatcccactagac 426
                                                                                                      gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                                                        9ctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 366
                                                                                                                                                                       ctggtttttattcttccctctctcatgttattaatccctcatatactgctagagaacttt 120
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/product= "Human transmembrane protein HP02000"
/note= "No stop codon given in the specification"
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100.0%; Pred. No. 7.8e-174;
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WPI; 2001-367057/38
                            Sun W;
                                               (META-) METABASIS THERAPEUTICS INC
                                                                           12-JUL-1999;
                                                                                                  12-JUL-2000; 2000WO-US18980.
                                                                                                                             18-JAN-2001.
                                                                                                                                                        WO200104283-A2
                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                           Human; organic anion transporter; hOAT; liver; kidney;
                                                                                                                                                                                                                                                                       membrane
                                                                                                                                                                                                                                                                                                             hOAT5 DNA.
                                                                                                                                                                                                                                                                                                                                06-AUG-2001 (first entry)
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                                                                                                                                                                                                                                                                       protein;
                                                                         99US-0143771.
                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                              /product- "hOAT5"
                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                               transport; organic anion; splice variant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAC85819-24 encode human organic anion transporter (hOAT) polypeptides. hOAT polypeptides are preferentially expressed in the liver and kidneys of humans. OAT's are membrane proteins that facilitate the transport of organic anions across the proteins that facilitate the transport of organic anions across the cell membrane. The mechanism of transport is thought to be a secondary or tertiary active transport involving exchange of another organic anion. hOAT2A and hOAT2B are thought to be splice variants as they are identical except at the C-terminal end. hOAT proteins and the DNA encoding them, may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate hOAT expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human organic anion transporter polypeptides,
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Local Similarity 66.2%;
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674 ggaggcatcataggtggccatgtctcagacaggtttgggcgaagatttattctcagatgg 733
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                     ggaggcatcataggtggccatgtctcagac-----
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- α	1754 aagaatotgootttgootgacaccatcaaggatgtggaaaatcaaaaaaaaaa	Дb
4	933aaaaaaaatctcaa	Qy
	1694 atcatttatggaatcttccccatcattggtggccttattgtcttcctcctaccagaaac	Db
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5	1454 tocattttggccaacacgtttgtgcccaaagaaatgcagaccctgcgtgtggctttggca :	Дb
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-	1394 acactaaatcatatgggccgtcgaataagccagatattgttcatgttcctggtgggcctt	Дb
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N	accatgcaggaggagctggatgcagcacagaccaaaactactgtgtgt l	Db
76	ttgtaagatccaccatgcaggaggagctggatgcaggaccaagaccaaaactactgtgtgt 8	Qy
ıμ	agaaaagttgcacgcacaaatggaataaagaatgctgaagaaaccctgaacatagag l	망
16	ttagaaaagttgcacgcacaaatggaataaagaatgctgaagaaaccctgaacatagag 8	Qy
_	ctgctcggtggttgataatcaccaataaactagatgagggcttaaaggca l	Дb
, φ	tggtggaatctgctcggtggttgataatcaccaataaactagatgagggcttaaaggca 7	Qy
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	734 tgtttgctccagcttgccattactgacacctgcgctgccttcgctcccaccttccctgtt 79	Db
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                                                                     09-AUG-2001.
                                                                                                                                                         cytostatic; gene therapy; vaccine; metastasis;
                                                                                                                                                                                               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24948
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                                                                                                                                 Homo sapiens.
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                                            Ruben SM;
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis .

WPI; 2001-483426/52

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AAAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) cc amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc contributy, and can be used in gene therapy and vaccine production. (I) cc activity, and can be used in gene therapy and vaccine production. (I) cc proteins and polynucleotides may be used in the prevention, diagnosis and cc treatment of diseases associated with inappropriate (I) expression. For cc treatment of they may be used to treat disorders associated with decreased cc example, they may be used to treat disorders associated with decreased cc example, they may be used to treat disorders in a patient's genome cc that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) cc supplement the patients own production of (I). Additionally, (I) cc supplement the patients own produce the secreted (I), by inserting cc polynucleotides may be used to prevent, and include acids into a host cell and culturing the cell to express the cc protein. (I) proteins and polynucleotides may be used to prevent, cc diagnose and treat immune/haematopoietic-related diseases, especially capacity and cancer metastases of haematopoietic antigen genomic cc to AAK87694 represent human immune/haematopoietic antigen genomic cc represent seniered in the exemplification of the present invention. AAK5492 to AAK5450 and AAM62169 cr patresent senieres used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1053 caccagaagggtttttttccctacaaccagcaagaacatatattagatacatgaatctca 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             933 aaaaaaaatotoaaggaaaaggoataaaaatgattgotacacaaaagtgaccaaaatttta 992
                                                                                                                                                                                                                                                                                                                                                                                                                                     1293 ctggtgtatgaagcaccatgtgatgaattcataaagttgcaaaagtcaaaacaatactgt
                                                                                                                                   536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1593 gtttacaatattataaagatattgttcaaattgaagggcaaaggccaggttcagcaattt 1652
                                             296
                                                                                                                                                                                                                                                                                                                                                                                                                416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTTGAGCAATCTGATATTTTTGGGAAGTCCTTTAAAAAGTTACAAATTTATCAATAAA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCAGAAGGGTTTTTTTCCCTACAACCAGCAAGAACATATATTAGATACATGAATCTCA
                                                                                                                                                                                                                              CATGATACTTTTGACATAATAAGCCATTGGAAAACGGAAAGATTAGATACTAAATAACAT 237
                                                                                                                                                                                                                                                         ACATGCAACCAGAAATCAAAATAAATCCAGAAATAGAGACCTATATAAATGCATTTAATA
                                                                                                                                                                                                                                                                                                                                             acatgcaaccagaaatcaaaataaatccagaaatagagacctatataaatgcatttaata
                                                                                                                                                                                                                                                                                                                                                                                                             CTGGTGTATGAAGCACCATGTGAATGAATTCATAAAGTTGCAAAAGTCAAAAACAATACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.3%; Score 773; DB 22; 100.0%; Pred. No. 9.1e-167;
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AAI AAI AAI AAI AAI AAI AAI AAI	Qy Db	ДD
AAK70138; 06-NOV-2001 (first entry) Human immune/haematopoietic antigen genomic sequence SEO ID Human; Immune/haematopoietic; immune/haematopoietic antigen Grostatic Gr	1653 tcaaactgtatgtacatttaataaataactataaattaaaaaa 	11111111111111111111111111111111111111
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08-SEP-200 14-SEP-200 14-SEP-200 14-SEP-200 14-SEP-200 14-SEP-200 14-SEP-200 14-SEP-200 25-SEP-200 25-SEP-200 27-SEP-200 29-SEP-200 20-CCT-2000 21-CCT-2000 20-CCT-2000 20-CCT-2000 20-CCT-2000 21-CCT-2000	08-SEP-20 08-SEP-20 08-SEP-20 08-SEP-20	08-SEP-20
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AXX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC arctivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC proteins and polynucleotides may be used in the prevention. For CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC used the activity of (I) by expressing inactive proteins or to CC used the activity of (I) by expressing inactive proteins or to CC used the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-derived cells. AAK64703 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC cancers and cancer metastases of haematopoietic antigen genomic to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK9490 and AAM82169 control of the present invention.
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17-NOV-2000;
17-NOV-2000;
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Best Local S
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08-DEC-2000;
08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 24950; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                    Sequence 782 BP; 241 A; 119 C; 105 G; 317 T; 0 other;
                                                            1113 attataattatggcattaatttgcattttatttcaaaattaacttgtggggacatgtaat 1172
                                                                                                                                                                                                      933 aaaaaaatctcaaggaaaaggcataaaaatgattgctacacaaaagtgaccaaatttta 992
                                                                                                                                                           993
                                                                                                                                                                                        775 AAAAAAATCTCAAGGAAAAGGCATAAAAATGATTGCTACACAAAAGTGACCAAATTTTA 716
                                                                                                                                             ATTATAATTATGGCATTAATTTGCATTTTATTTCAAAATTAACTTGTGGGGACATGTAAT 536
                                                                                                                                                                                                                                                                        h 44.6%;
Similarity 99.9%;
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; 2000US-0249297.
; 2000US-0249299.
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2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251869.
2000US-0251869.
2000US-0251999.
2000US-0251999.
2000US-0254997.
2001US-0259678.
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2000US-0250391.
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2000US-0249264.
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                                                                                                                                                                                                                                                          Score 761; DB 22; Length 782; pred. No. 5e-164; 0; Mismatches 0; Indels
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AAK70137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 TTACTAGTAGATAAGATGATTCAGAAACAAAAGAAAATCACAGAATTAGGATGTGGCTGG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1473 tgactatototttgtaaatacagtoactaaatgatgttagttacttttocatggtggaat 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355
                                                                                                                                                                                                                                                                                                                                                                                                      1653 tcaaactgtatgtacatttaataaaataactataaattaaaaaaattatattc 1705
                                                                                                                                                                                                                                                                                                                                         AAK70137 standard; DNA; 782 BP
                 16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                            cytostatic; gene therapy; vaccine; metastasis; ds
                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24949.
                                                                                                                                                                                                                                                                                                  06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                      AAK70137;
                                                                                                                                                                                                                                                                                                                                                                                                                                  116 GTTTACAATATTATAAAGATATTGTTCAAATTGAAGGGCAAAAGGCCAGGTTCAGCAATTT
                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                            Homo sapiens.
                                                                                                            24-FEB-2000;
02-MAR-2000;
                                                                                                                                            31-JAN-2000;
                                                                                                                                                                17-JAN-2001; 2001WO-US01354.
                                                                                                                                                                                                                                                                                                                                                                                          56 TCARACTGTATGTACATTTAATAAAATAACTATAAATTAAAAAATTATATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATGATACTTTTGACATAATAAGCCATTGGAAAACGGAAAGATTAGATACTAAATAACAT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acatgcaaccagaaatcaaaataaatccagaaatagagacctatataaatgcatttaata 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGTGTATGAAGCACCATGTGATGAATTCATAAAGTTGCAAAAGTCAAAACAATACTGT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATGCAACCAGAAATCAAAATAAATCCAGAAATAGAGACCTATATAAATGCATTTAATA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                            gtttacaatattataaagatattgttcaaattgaagggcaaaggccaggttcagcaattt 1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0190076.
2000US-0198123.
 2000US-0205515
2000US-0209467
2000US-0214886
2000US-0215135
2000US-0216647
2000US-0216880
2000US-0217487
2000US-0217487
2000US-0217487
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2000US-0180628.
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2000US-0218290 2000US-0220963

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic proteins and polynucleotides may be used in the prevention. (I) treatment of diseases associated with inappropriate (I) expression. For expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to freat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to production of (I). Additionally, (I) the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent,
                                                                                                                                                                                                                                                                                                                                      17-NOV-2000

17-NOV-2000

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17-NOV-2000

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17-NOV-2000

01-DEC-2000

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08-DEC-2000
                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                    useful for metastasis
                                                                                                                                                                                                                        Nucleic acids encoding
                                                                                                                                                                                                                                                   WPI; 2001-483426/52.
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17-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                HUMAN GENOME SCI INC
                                                                                                                                                                                                      preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                         Barash SC,
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2000US-0251868.
2000US-0251869.
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2000US-0249245
2000US-0249264
2000US-0249265
2000US-0249265
2000US-0249299
2000US-0249299
2000US-0249390
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2000US-0251990
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2000US-0249215.
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2000US-0249209.
2000US-0249210.
2000US-0249211.
2000US-0249211.
2000US-0249213.
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2000US-0246609.
2000US-0246610.
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2000US-0246526
2000US-0246527
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08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 12-SEP-2000; 14-SEP-2000;

2000US-023943 2000US-0230437 2000US-0231243 2000US-0231244 2000US-0231413 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231416 2000US-0232081 2000US-023298 2000US-023298 2000US-023298 2000US-023298 2000US-023298 2000US-0232401 2000US-0233401 2000US-0233401 2000US-0233401 2000US-0233401 2000US-0233401 2000US-023401
18-AUG-2000)
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2000US-0226888 2000US-0227182 2000US-0227182 2000US-0228924 2000US-0229287 2000US-0229343 2000US-0229344 2000US-0229345 2000US-0229513 2000US-0229513

2000US-0225267. 2000US-0225268. 2000US-0225270.

02-0CT-2000 02-0CT-2000 02-0CT-2000 02-0CT-2000 13-0CT-2000 13-0CT-2000 20-0CT-2000
2000US-0240960 2000US-0241221 2000US-0241785 2000US-0241787 2000US-0241787 2000US-0241808 2000US-0241809 2000US-0241826 2000US-0241826 21-SEP-2000 25-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000

2000US-0235836 2000US-0236327

200005-0236367.

2000US-0236368. 2000US-0236369. 2000US-0236370. 2000US-0236802. 2000US-0237037.

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                                      AAF55043;
                                                                              AAF55043 standard; DNA; 1316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attataattatggcattaatttgcattttatttcaaaatttaacttgtggggacatgtaat 1172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACCAGAAGGGTTTTTTTCCCTACAACCAGCAAGAACATATATTAGATACATGAATCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTACTAGTAGATAAGATGATTCAGAAAACAAAAGAAAATCACAGAATTAGGATGTGGCTGG
                                                                                                                                                                                                                                                                              gtttacaatattataaagatattgttcaaattgaagggcaaaggccaggttcagcaattt 1652
                                                                                                                                                                                                                                                                                                                                        TTTAATTACTTTTCTTTGTAA-TTTTCTCTCTGTATATTTTAAACAAATAGCTGGTATA 117
                                                                                                                                                                                                                                                                                                                                                               tttaattactttttctttgtaatttttctctctctgtatatttttaaacaaatagctggtata 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                           ACATGCAACCAGAAATCAAAATAAATCCAGAAATAGAGACCTATATAAATGCATTTAATA
                                                                                                                                                                               tcaaactgtatgtacatttaataaaataactataaattaaaaaattatatttc 1705
                                                                                                                                                                                                                                                         GTTTACAATATTATAAAGATATTGTTCAAATTGAAGGGCAAAGGCCCAGGTTCAGCAATTT 57
                                                                                                                                                                                                                                                                                                                                                                                                                        TGACTATCTCTTTGTAAATACAGTCACTAAATGATGTTAGTTTCTTTTCCATGGTGGAAT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGATACTTTTGACATAATAAGCCATTGGAAAACGGAAAGATTAGATACTAAATAACAT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 759.4;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 1.1e-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Query Match
Best Local
Matches
                                                                                                    The present sequence encodes a calcium channel transport polypeptide. The polynucleotides, polypeptides, and antibodies are useful for preventing, treating, or ameliorating diseases associated with anomalies in calcium trafficking across the plasma membrane. They are used to diagnose, detect and treat or prevent diseases or conditions such as neural disorders (e.g. HIV-induced dementia), immune system disorders (e.g. rheumatoid arthritis), muscular disorders (e.g. muscle contractile dysfunction), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. arrhythmias), renal disorders, proliferative disorders, and/or cancerous diseases and conditions (e.g. lung carcinoma or breast cancer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferative disorder; cancer; lung carcinoma; breast cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rheumatoid arthritis; muscular disorder; muscle contractile dysfunction; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; arrhythmia; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calcium channel transport polypeptide; neural disorder; HIV-induced dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of a calcium channel transport polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neural disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-1999; 99US-0145958.
18-AUG-1999; 99US-0149446.
14-MAR-2000; 2000US-0189064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200108635-A2.
                                                                                                                                                                                                                                                                                                                                            across the plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAB67466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUL-2000; 2000WO-US20392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2001
                                                                                                                                                                                                                                                                                                           Claim 1; Page 254; 259pp; English.
                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid useful for diagnosing, detecting, or treating or preventing diseases associated with anomalies in calcium trafficking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                          Sequence 1316 BP; 458 A; 227 C; 237 G; 394 T; 0 other;
 Local Sin
                                                                                                                                                                                                                                                                                                                                                                                                                              2001-138604/14.
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                 Similarity
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 Conservative
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/product= "calcium channel transport polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36..341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shi Y;
                 43.3%;
98.7%;
   0;
                 Score 738.6; DB 22
Pred. No. 7.5e-159;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                calcium trafficking;
                                    DB 22;
      Indels
                                    Length 1316;
      1;
        Gaps
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03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                              myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                        05-FEB-2001; 2001WO-US03800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                       antifungal; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein homologue-encoding cDNA, SEQ ID NO:752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA08976 standard; cDNA; 1353 BP
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                                                                                                                                                                                                                                                                                                                                                                                                         osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                   antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1005
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CC haematopoiesis regulatory activity; tissue growth activity;

CC haematopoiesis regulatory activity; tissue growth activity;

CC chemotactic or chemokinetic activities; haemastatic, thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be

CC dispolated in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, haematopoletic discorders (e.g., myeloid or lymphoid cell

CC cancers, chronic inflammatory conditions (e.g., asthma or arthritis),

CC arterial ischaemia, bone discorders (e.g., myeloid or lymphoid cell

CC vascular growth. Polypeptides involved with tissue regeneration and

CC healing (e.g., of burns, inclisions and ulcers), while those with

CC polypeptides with growth factor activity may be used to promote wound

CC promote cell growth. For example, such polypeptides may be used to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC may also be used in the diagnosis of the above conditions, and indreg

CC may also be used in the diagnosis of the above conditions, and indreg

CC conditions, and indreg

CC conditions and uncers in a cell cultures to

CC may also be used in the diagnosis of the above conditions, and in drug

CC conditions and uncers in a cell cells

CC may also be used in the diagnosis of the above conditions, and in drug

CC movel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention management of the protein of the invention management of the polypeptides of the invention of the polypeptides of the polypeptides of the invention of the polypeptides of the invention of the polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences ABB10981-ABB12330 represent 1350 novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides, an coding them. The
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Sequence 1353 BP; 349 A; 298 C; 315 G; 391 T; 0 other;

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tggcctttgaggagctcttgagtcaagttggaggccttggggagatttcagatgcttcatc
                                        ttgaacttatctccgtaaagccattgtgcctcctcttgggggtcacgtgttcacaatcaa
                                                        ttgaacttatctccgtaaagccattgtgcctcctcttgggggtcacgtgttcacaatcaa
                                                                                                               attgatgogaggatcaatacaagcttaatttgaattaataaaaggaaatattttctccct 127
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                                                                                                attgatgcgaggatcaatacaagcttaatttgaattaataaaaggaaatattttctccct
                                                                                                                                                      gaggaagctctttccactacggctgtattgcactggtgagtccgggcccatggatgagaa
                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                 40.38;
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                                                                                                                                                                                                                              Score 687; DB 22; Pred. No. 4.5e-1
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI59215 standard; cDNA; 1375 BP
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                                                                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 1418.
                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-2001 (first entry)
 Tang YT,
Wang J,
                                                                                                                      21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
                                                                                                                                                                                                                                WO200153312-A1
                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                 leukaemia; ss.
                                                                                                                                                                             26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                      26-JUL-2001
                                                                                                   19-JUL-2000;
03-AUG-2000;
                                      (HYSE-) HYSEQ INC.
                                                                            14-SEP-2000;
19-OCT-2000;
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  Wang
  Liu C,
Wang Z,
                                                                                                  2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
                                                                 2000US-0693036.
2000US-0727344.
                                                                                          2000US-0662191.
    Asundi V,
Wehrman T,
     Chen R,
        Ma Y,
Xue AJ,
         Qian XB,
Yang Y,
          Ren F, 'S' Zhang J;
                        Wang
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, the immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity a polypeptide or polynucleotide in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and system such as localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system disease, amyotrophic Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic activiny inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, and throwards activity, architits and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1418; 10078pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 ccctttgaacttatctccgtaaagccattgtgcctcctcttggggggtcacgtgttcacaa 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 catctggtttttattcttccctccatgttattaatccctcatatactgctagagaac
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                                                                                                                                                                       cacctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtggatggc 543
                                                                                                                                                                                                                            gactcaaacatgaggccagagaagtgtcgtcgctttgttcatcctcagtggcagctcctt 584
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gactctcaatcactgacttcagtggctaaatttgtattcatggctggaatgatggtggga
                  gattatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtggga
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Pred. No. 2.2e-81;
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         The present sequence is transporter and ion channel-10 (TRICH-10) cDNA. TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth neurological disorders including Alzheimer's disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar
disorder, dementia, depression, epilepsy, ischaemic cerebrovascular
                                                                                                                                          Claim 5; Page 147; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-2000;
21-JAN-2000;
28-JAN-2000;
02-FEB-2000;
                                                                                                                                                                                               Novel human transporter and ion channel proteins useful for treating
                                                                                                                                                                                                                                                 P-PSDB; AAE04897
                                                                                                                                                                                                                                                            WPI; 2001-418042/44.
                                                                                                                                                                                                                                                                                                            Hillman JL,
                                                                                                                                                                                                                                                                                                                        Baughn MR, Burford N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; vaccine; arrhythmia; Huntington's disease; Parkinson's disease; AIDS; anxiety; stroke; demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease; rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; wilson's disease; infertility; Cushing's disease; sickle cellaneonary artery stenosis; nootropic; Addison's disease; malabsorption syndrome; hypercholesterolaemia; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-2000; 2000WO-US35095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200146258-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-2001 (first entry)
                                                                                                                                                                                       preventing transport, neurological,
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2000US-0177332.
2000US-0178572.
2000US-0179758.
                                                                                                                                                                                                                                                                                                           Azimzai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0172000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Human TRICH-10 protein"
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                                                                                                                                                                                                                                                                                                    Au-Young J, Lu DAM,
, Yue H, Nguyen DB,
                                                                                                                                                                                          muscle
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Yao MG,
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Gandhi AR;
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RESULT 12 AAC61892

AAC61892 standard; cDNA;

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725 ggcatcctaggcggtcatttatcagacaggt 755
                     664 ggcatcataggtggccatgtctcagacaggt 694
                                                                                      604 gattatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease, stroke, cerebral neoplasms, plck's disease, Huntington's disease and Parkinson's disease, demyelinating disease, mental disorders including mood, anxiety, Schizophrenia and seasonal affective disorder, dermatomyositis including cardiomyopathy, myocarditis, polymyositis, arrhythmias and asthma and immunological disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies, syndrome, systemic lupus erythematosus and other diseases including srickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary glucose-galactose mellabsorption syndrome, hypercholesterolaemia, cancers infections. TRICH DNA is useful in gene therapy and in diagnostic
                                                                                                                                                            544 tgggtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgt
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Pred. No. 2.5e-81;
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xx AAC61879-93 encode secreted human proteins. The secreted proteins are cc useful in assays to determine their biological activities. The proteins cc useful in assays to determine their biological activities. The proteins cc earlies are inserted proteins. The polynucleotide molecules can be used as comparison to proteins and antibodies are useful in diagnosis and treatment of biomarkers for tissues or chromosomes and to elicit immune responses. The cc diseases associated with altered expression of these proteins. The cc diseases associated with altered expression of these proteins. The cc disorders, stem cell disorders, osteoporosis or osteoparthritis, burns, cc disorders, stem cell disorders, central and peripheral nervous cc inclsions, ulcers, periodontal diseases, central and peripheral nervous cc system diseases and neuropathies, for healing fractured bones and to cc proteins are also useful for gut protection or regeneration, for the creatment of lung or liver fibrosis, for stimulating blood cell creatment of lung or liver fibrosis, for stimulating blood cell of bone marrow transplantation patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted protein; platelet disorder; stem cell disorder; osteoporosis; osteoarthritis; burn; inclsion; ulcer; periodontal disease; neuropathy; nervous system disease; bone growth; cosmetic plastic surgery; qut protection; gut regeneration; fibrosis; cancer; the protection; disease; bone growth; cosmetic surgery; put regeneration; fibrosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding a human secreted protein.
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20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel secreted human proteins useful for stimulating blood cell generation in patients receiving cancer chemotherapy, treating bone marrow transplantation patients and for healing fractured bones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 71-72; 74pp; English.
                                                                                                                                                                                                                                                        Sequence 2027 BP; 530 A; 501 C; 459 G; 537 T; 0 other;
                                                                                                           124 cootttgaacttatotoogtaaagccattgtgcotootottgggggfcacgtgttcacaa 183
184 tcaatggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgctt
                                                                                                                                                                                          Match 23.28; Local Similarity 76.78;
                                                                                                                             64 agaaattgatgogaggatcaatacaagcttaatttgaattaataaaaggaaatattttct 123
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                                               ctctttgaacctctctggatacagtcattttgcctctacttgaggatcaactgttcaacc 266
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99US-0150054.
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                                                                                                                                                                                          0;
                                                                                                                                                                                                        Score 395.8; DB 2
Pred. No. 1.3e-80;
                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                        Human; organic anion transporter; hOAT; liver; kidney;
                                                                                                                                                                                                                                                                                                                  hoat4 DNA
                                                                                                                                                                                                                                                                              membrane protein; transport; organic anion; splice variant; ds.
                                                                                                                                                                                                                            CDS
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                                                                                                                                                                              WO200104283-A2
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                                                                                                                                  12-JUL-2000; 2000WO-US18980.
                                                                                                                                                         18-JAN-2001.
                                                                                                             12-JUL-1999;
                                                                                       (META-) METABASIS THERAPEUTICS INC
Nucleic acids encoding human organic anion transporter polypeptides, useful in gene therapy procedures \dot{\ }
                                            WPI; 2001-367057/38.
                               P-PSDB; AAB47275
                                                                   Sun W;
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                                                                                                                   9905-0143771.
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                                               AAI61001 standard; cDNA; 1132 BP.
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                                                                                                       713 ggaggcatcttaggcgttcatttatcagacaggt 746
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                                                                                                                                                               601 tgtgattatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtg 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAC85819-24 encode human organic anion expressed in the liver and kidneys of humans. OAT's are preferentially proteins that facilitate the transport of organic anions or tertiary acclive transport involving exchange of another accordary identical except at the C-terminal end. hoar as a secondary identical except at the C-terminal end. hoar proteins and the DNA of diseases associated with inappropriate hOAT expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 tcaatggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgctt 243
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                                                                                                                                                                                                                                                                                                                                                           totgacaatgacactggggccctcagccaagatgcactcttgagaatctccatcccactg 472
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                                        439 ccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcacctgaatgggact 498
                                                                                                                                                                                                                                                      the encoded polypeptides (AAMA3203) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful gene therapy. A composition containing a polypeptide or polynucleotide system, such as peripheral nervous injuries; peripheral nervous alzheimer's, Parkinson's disease, Huntington's diseases, such as utilisation of the activitices such as: Immune system diseases, such as utilisation of the activity, chemotactic/Chemokinetic activity, hemotactic/Chemokinetic activity, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S. diseases
                                                                                         379 ggaatcotcagtgaagatgccotcttgagaatctotatcccactagactcaaatctgagg 438
                                                                                                                                                                                                    Sequence 1132 BP; 274 A; 265 C; 285 G; 305 T; 3 other;
                                                                                                                                                                                                                              C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
                        87 ccagagaagtgtcgtcgctttgttcatcctcagtggcagctccttcacctgaatgggacc 146
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 4990; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
Wang J,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAM41845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE~) HYSEQ INC.
                                                                              9999ccctcagccaagatgcactcttgagaatctccatcccactggactcaaacatgagg 86
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                                                                                                                                                              h 13.7%;
Similarity 83.5%;
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Wang Z,
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); 2000US-0620312.
); 2000US-0653450.
); 2000US-0662191.
); 2000US-0693036.
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Pred. No. 1.7e-43;
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Yang Y,
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                                                                                               Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -
                                                                        Claim 4; Page 252-257; 563pp; English.
                                                                                                                                                                                                                                                                        06-JAN-2000; 2000JP-0000585.
06-JAN-2000; 2000JP-0000588.
11-JAN-2000; 2000JP-0002299.
03-FEB-2000; 2000JP-0026862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contraceptive; antiinfertility; antiinflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
                                                                                                                                                                                                                         (SAGA )
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/note= "CDS is specifically is claimed in claim 3"
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                       635 tcctacttctgactggaatgctgggtgggaggcatcataggttggccatgtctcagacaggt 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         into a host cell and culturing the cell to express the protein. The polynicleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional
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Local Similarity 62.8%;
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Pred. No. 4.3e-40;
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Search completed: July Job time: 6280 sec 1,

The present sequence is human protein with hydrophobic domain encoding cDNA clone HP03613: The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids

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OM nucleic - nucleic search, using sw model
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AP001880 Homo sapi
AC025409 Homo sapi
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AB051836 Rattus no
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ALIGNMENTS

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DEFINITION
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AX074150
AX074150.1 GI:12710362
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                                                                          organic anion transporter genes and proteins patent: WO 0104283-A 6 18-JAN-2001; Metabasis Therapeutics Inc. (US)
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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CGTCAG	14 GGTGCCCTTAGTATTGGACAGATAATCCTGGGAGGCTTGGCT	91	54 TTGCCCATTACTGAGTGCATTACCA	ACGCTTCTTGGCAGGTTTTTCTTCCATGATCAT	CCTTCGCTCCACCTT	TTGCCATTACTGACACCTGCGCTGCGTTGCCTTTCCCTTT		agac	614 TGTGATTATCAGTCACTGAAATCAGTGGTTCAATTTCTATTTTTTTT	tgattatcagtcactgaaatcagtggttcaattgTGTGACTAAGTGGGACCTGG	554 GCTGGGTATATGATCAAAGCTACTTCCCTTCGACCATTCT	41 99ct999tatatgatcaaagctacttactt		TAGACTCAAATCTGAGG	21 ctagactcaaatctgaggccagagaagtgtcgttgtccatcca	374 GGATCTGGTAATGAAACTGGAAATCCTCAGTGAAGATGCCTCTTTGAGGAGATCTCTTTIIIIIIIIII	gatetggtaatgaaactggaatcotcactericeTGGGTCCACATGCTGGACAATAATAC	314 AACTTTGCTGCAGCCATTCCTGGTCATCCTTTTTTTTTT	actttgctgcagccattcctqqtca+ca+ca+	254 CTTCATCTGGTTTTTATTCTTCCCCTCTTTTTTTTTTTT	tteatetggttttattetteetetetetetetetetetet	aga	aatcaatggcctttgaggaggtct.	134 TCTCCCTTTGAACTTATCTCCGTAAACCCATTGTCTTTTTTTT	121 totocotttgaacttatotccgfaaaccatta	74 A	61 atgagaaattgatgogaggatcaattgatgogaggtcaattaattaattaattaattaattaattaattaa	14 AAGAACTGAGGAAGCTCTTTCCACTACTACTACTACTACTACTACTACTACTAC	1 aagaactgaggaaggtgttttccatta	801 No.

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                                                                                     TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 164809) Birren,B., Linton,L., Nusbaum,C. and Lander,E. Birren,B., Cintomosome 11, clone CTD-3110P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boyuslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., K., 
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                                                                                                Sougnez, C., Sencer, B., Stange-Thomann, N., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zambek, L., Zinmer, A. and Zody, M.
Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
Smit, M.F.A. & Genome washington.edu/RM/RepeatMasker.html
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
....- Project Information
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3441 3540: gap of 100 bp
3441 3540: gap of 1340 bp in length
3541 4980: contig of 1788 bp in length
4881 4980: gap of 100 bp
6769 6868: gap of 100 bp
8318: contig of 1450 bp in length
6869 8318: contig of 1628 bp in length
10047 10146: gap of 100 bp
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3441 3540: gap of
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1170 2379; contig of 1210 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                /note="assembly_fragment"
                                                                                                                                                                                      /note="assembly_fragment"
                                                                                                                                                                                                                                        /clone_lib="CITD Human BAC"
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15164: contig of 2609 bp in length
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of 961 bp in length
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ORIGIN
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26437 AATGCATTTAATACATGATACTTTTGACATAATAAGCCATTGGAAAACGGGAAAGATTAGA 26378
                                                                                       26557 AGGATGTGGGTGGTGTGTATGAAGCACCATGTGATGAATTCATAAAGTTGCAAAAGTC 26498
                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                26617 ATTTATCAATAAATTACTAGTAGATAAGATGATTCAGAAACAAAAGAAAATCACAGAATT 26558
                                                                                                                                                                                                                           1280 aggatgtggctggctggtgtatgaagcaccatgtgatgaattcataaagttgcaaaagtc 1339
                                                                                                                                                                                                                                                                      1220 atttatcaataaattactagtagataagatgattcagaaacaaaagaaaatcacagaatt 1279
                                                                                                                                                                                                                                                                                                                  26917 TTGTTTTCCAGAAAAAAAATCTCAAGGAAAAGGCATAAAAATGATTGCTACACAAAAG 26858
                                                                                                                                                                                                                                                                                                                                                                         920 tggtatttttgagaaaaaaatctcaaggaaaaggcataaaaatgattgctacacaaaag 979
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Match
Local Similarity 99.1%; Pred. No. 1.5e-141;
es 779; Conservative 0; Mismatches 7; Indels 0;
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103069. .164809
/note="assembly_fragment"
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3541. .4880
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                                82586 CAGGAAAAGAACACCAGAAGGGTTTTTTTCCCTACAACCAGCAAGAACATATATTAGA 82645
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                                                                                            JOURNAL
1100 tacatgaatctcaattataattatggcattaatttgcattttatttcaaaattaacttgt 1159
                                                1040 caggaaaggaacacaccagaagggtttttttccctacaaccagcaagaacatatattaga 1099
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                                                                                                           920 tggtatttttgagaaaaaatctcaaggaaaaggcataaaaatgattgctacacaaag 979
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Similarity 99.1%; Score 774.8; DB 9; Length 169776;
779; Conservative 0; Mismatches 7; Indels 0; (
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48281 a 32818 c 33507 g 55170 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Only in DataBase (2000) In press 2 (bases 1 to 169776)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y., Homo sapiens genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens genomic DNA, chromosome 11q, clone;CTD-3110p2
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                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/chromosome="11"
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Location/Qualifiers
1. .169776
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           COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83126 AATAGCTGGTATAGTTTACAATATTATAAAGATATTGTTCAAATTGAAGGGCAAAGGCCA 83185
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                                                                                                                                TITLE
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                                                                                                             JOURNAL
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APU02367

Homo sapiens chromosome 11 clone RP11-151E18 map 11q, WORKING DRAFT
SEQUENCE, 9 unordered pieces
                                                                                                                            To bases 1 to 166848)

1 (bases 1 to 166848)

Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
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                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                          Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (Riksasto, Sagamihara, Kanagawa 228-8555, Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, Japan (E-mail:hattori@gsc.riken.go.jp, Tel:81-42-778-9923, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                            HTGS_PHASE1;
                                                                                                                                                                                                                                                                                                                                     sapiens DNA, clone:RP11-151E18.
Center: RIKEN Genomic Sciences Center(GSC)
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Contact: hattori@gsc.riken.go.jp
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73754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 bp
152955 161965; contig of 9011 bp
161966 162065; gap of 100 bp
162066 165410; contig of 3345 bp
165411 165510; man of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165411 165510: gap of 100 k
165511 166848: contig of 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       project Information
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73653 contig of
99297 contig of
123005 contig of
140640 contig of
152854 contig of
161965 contig of
165410 contig of
166848 contig of
                                                                                                                                               /note="assembly_fragment"
73754. 99207
                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
99398. .123005
/note="assembly_fragment"
123106. .140640
                                                                                                                                                                                                                                                                                                                            /clone="RP11-151E18"
                                                                                                                                                                                                                                              /note="assembly_fragment"
                                                                                                          /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39293: contig of 39293 bp in length
393: gap of 100 bp
73653: contig of 34260 bp in length
                                                                                                                                                                                                                                                                                                   .39293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .166848
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length
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HTG 07-JUL-2000

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35851 TATTTC 35846
                                                                                                                                                                           35911 GGTTCAGCAATTTTCAAACTGTATGTACATTTAATAAAATAACTATAAAATTAAAAAATTA 35852
                                                                                                                                                                                                                                                              35971 AATAGCTGGTATAGTTTACAATATTATAAAGATATTGTTCAAATTGAAGGGCAAAGGCCA 35912
                                                                                                                                                                         1700 tatttc 1705
                                                                                                                                                                                                                                                                                                                                                  36030 TCCATGGTGGAATTTTAATTACTTTTTTTTTTTTTAAA-TTTTCTCTCTGTATATTTTTAAACA 35972
                                                                                                                                                                                                1580 aatagctggttatagtttacaatattataaagatattgttcaaattgaagggcaaaggcca 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36150 AATGCATTTAATACATGATACTTTTGACATAATAAGGCCATTGGAAAAACGGAAAGATTAGA 36091
                                                                                                                                                                                                                                                                                                                                                                          1520 tocatggtggaattttaattactttttctttgtaattttctctctgtatattttaaaca 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                             36210 AAAACAATACTGTACATGCAACCAGAAATCAAAATAAATCCAGAAATAGAGACCTATATA 36151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1400 aatgcatttaatacatgatacttttgacataataagccattggaaaacggaaagattaga 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36270 AGGATGTGGCTGGCTGTATGAAGCACCATGTGATGAATTCATAAAGTTGCAAAAGTC 36211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36330 ATTTATCAATAAATTACTAGTAGATAAGATGATTCAGAAACAAAAGAAAATCACAGAATT 36271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36390 GGGGACATGTAATCTCTTGAGCAATCTGATATTTTTGGGAAGTCCTTTAAAAAGTTACAA 36331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1340 aaaacaatactytacatycaaccagaatcaaaataaatccagaaatagagacctatata 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1280 aggatgtggctggctggtgtatgaagcaccatgtgatgaattcataaagttgcaaaagtc 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36450 TACATGAATCTCAATTATAATTATGGCATTAATTTGCCATTTTATTTCCAAAATTAACTTGT 36391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36510 CAGGAAAAGAACACACAGAAGGGTTTTTTTCCCCTACAACCAGCAAGAACATATATTAGA 36451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1160 ggggacatgtaatctottgagcaatctgatatttttggggagtcotttaaaaagttacaa 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1100 tacatgaatctcaattataattatggcattaatttgcattttatttcaaaattaacttgt 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36630 TTGTTTTTCCAGAAAAAAAATCTCAAGGAAAAGGCATAAAAATGATTGCTACACAAAAG 36571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1040 caggaaaagaacacaccagaagggttttttttccctaccaccagcaagaacatatattaga 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        980 tgaccaaattttaagaagccttcatgagctgattggtggggaaattcagaagaagaata 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           920 tggtatttttgagaaaaaaatctcaaggaaaaggcataaaaatgattgctacacaaaag 979
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Local Similarity 99.0%; Pred. No. 3.2e-139;
les 778; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55669 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="assembly_fragment clone_end:SP6 vector_side:left"
165511. 166848
/note="assembly_fragment"
32391 c 31923 g 46064 t 801 others
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152955...161965
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140741. .152854
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AUTHORS
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AC073256/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name; H_NH0204X20

Sequencing vector: M13; 1008
Chemistry vector: plasmid; 08
Chemistry: Dye-primer ET; 1008 of reads
Assembly program: phrap; version 0.990319
Consensus quality: 15740 bases at least 040
Consensus quality: 15740 bases at least 040
Consensus quality: 15094 bases at least 040
Insert size: 161080; agarose-fp
Onality roversace: 4 62 in one has 020
Consensus quality: 15740 bases at least 030
Consensus quality: 163054 bases at least 040
Consensus quality: 163054 bases at least 040
Consensus quality: 163054 bases at least 030
Cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently * consists of 20 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouality coverage: 4.62 in 020 bases; agarose-fp quality coverage: 4.50 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center Code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-JUN 2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
On Jun 16, 2000 this sequence version replaced qi:8468975
                                                                                     19899
19999
24951
25051
30350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 170682) Waterston, R.H.
                                                                                                                                                                                            15817
15917
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11646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 11 clone RP11-204K20, WORKING DRAFT
SEQUENCE, 20 unordered pieces.
AC073256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE1; HTGS_DRAFT.
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2301
3482
3582
4833
4933
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15916: gap of unknown length
19898: contig of 3982 bp in length
19998: gap of unknown length
24950: contig of 4952 bp in length
25050: gap of unknown length
30349: contig of 5299 bp in length
36461: contig of 6012 bp in length
36561: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project
                                                                                                                                                                                                                                                                                      2200: contig of 2200 bp in length
2300: gap of unknown length
3481: contig of 1181 bp in length
4832: gap of unknown length
4932: gap of unknown length
6630: contig of 1251 bp in length
6630: contig of 1698 bp in length
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                                                                                                                                                                                                                        6: contig
                                                                                                                                                                                                                                                            gap of unknown contig of 4815
                                                                                                                                                                                                                                                gap of
                                                                                                                                                                                                                        t unknown
g of 4171
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bp in length
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В δõ 밁

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BASE COUNT

Matches Query Match

В

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В Ş В QΨ 밁 δõ B Qγ

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FEATURES
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     Query Match
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43194
43294
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82743
                                                                     /note="assembly_name:Contig27"
ture 144600 ...170682
/note="assembly_name:Contig28"
51522 a 33360 c 33713 g 50161 t 1
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2301. .3481
/note="assembly_name:Contig10"
3582. .4832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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94996: contig of 12254 bp in length
95096: gap of unknown length
108127: contig of 13031 bp in length
108227: gap of unknown length
127050: contig of 18823 bp in length
127150: gap of unknown length
144499: contig of 17349 bp in length
144599: gap of unknown length
144599: gap of unknown length
170682: contig of 26083 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_name:Contig13"
11646. 15816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-204K20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig15"
19999. .24950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3582. .4832
/note="assembly_name:Contigl1"
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                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_name:Contig18" 36562. .43193
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82743 94996
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                                                                                                                                                                                                              /note="assembly_name:Contig25
                                                                                                                                                                                                                                         /note="assembly_name:Contig24"
44.6%;
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                                                                                                                                                                     .127050
                                                                                                                                                                                                                                    10812
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Score 761.2; DB 2;
Pred. No. 6.5e-139;
                                                                                    1926 others
                     Length 170682;
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Best Local Similarity

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Db 134491 TTGTTTTCCAGAAAAAAAATCTCAAGGAAAAGGCATAAAAATGATTGCTACACAAAAG 134432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 134251 GGGGACATGTAATCTCTTGAGCAATCTGATATTTTTGGGAAGTCCTTTAAAAAGTTACAA 134192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 134191 ATTTATCAATAAATTACTAGTAGATAAGATGATTCAGAAACAAAAGAAAATCACAGAATT 134132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 777; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 134071 AAAACAATACTGTACATGCAACCAGAAATCAAAATAAATCCAGAAATAGAGACCTATATA 134012
                                                                                                                                                                                                                                                                                                                                                                                                                             Db 134011 AATGCATTTAATACATGATACTTTTGACATAATAAGCCATTGGAAAACGGAAAGATTAGA 133952
                                                                                                                                                                                                                                                                                                                                                                           Db 133832 AATAGCTGGTATAGTTTACAATATTATAAAGATATTGTTCAAATTGAAGGGCAAAGGCCA 133773
                                                                                                                                                                                                              Db 133712 TATTTC 133707
                                                               SOURCE
                                                                                                                                 DEFINITION
                                                                                                                                                            AP000596/c
                                                                               KEYWORDS
                                                                                                         ACCESSION
             REFERENCE
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                                                                                                           LLDZ/3 DP DNA linear HTG 30-MAY-20 DNA sapiens chromosome 11 clone XXpac-662A14 map 11g13, WORKING DRAFT SEQUENCE, 29 unordered pieces. APO00596
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 116273)
                                                                                               AP000596.2 GI:8118802
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
                                                                HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:XXpac-662A14.
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* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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110942 112367; contig of 1426 bp in length

112368 112467; gap of 100 bp

112468 113665; contig of 1198 bp in length

113666 113765; gap of 100 bp
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99845 101153: con
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73440 73939: gap of 100 bp
73940 77366: contig of 3427 bp in length
77367 77466: gap of 100 bp
77467 80065: contig of 2599 bp in length
80166 80165: gap of 100 bp
80166 803825: contig of 3660 bp in length
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44799 49514; contig of 4716 bp in length
49515 49614; gap of 100 bp
49615 55534; contig of 5920 bp in length
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55635 60136: conf
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44799. .49514
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/db_xref="taxon:9606"
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/map="11q13"
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114974: contig of 1209
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10841: contig of 2212 bp in length
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08529: contig of 1929 bp in length
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86777: contig of 2852 bp in length
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65623: contig of 5387 bp in length
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44698: contig of 6460
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49615. .55534
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70203. .71387
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Query Match 34.5%; Score 588; DB 9; Best Local Similarity 100.0%; Pred. No. 3.8e-10 Matches 588; Conservative 0; Mismatches 0
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1 (bases 1 to 160945)

1 (bases 1 to 160945)

1 (bases 1 to 160945)

Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Homo sapiens genomic DNA

Published Only in Database (2001) In press

2 (bases 1 to 160945)

2 (bases 1 to 160945)

3 (bases 1 to 160945)

4 Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Charlet Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens genomic DNA, chromosome 11q, clone:RP11-614K12
                                                                                                                                                                                                                                                                                    Submitted (16-MAR 2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Vokohama, Kanagawa 230-0045, Japan (P-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Aug 27, 2001 this sequence version replaced gi:13383333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete sequence.
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                                                                                                                            46743 a 31738 c 32047 g 50417
                                                                                                                                               /clone="RP11-614K12"
                                                                                                                                                                                                                                                    1. .160945
                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                    /map="11q"
                                                                                                                                                                                      /chromosome="11"
                                                                                                                                                                                                                                                                       Location/Qualifiers
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3.8e-105;

Indels

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Gaps

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 144204 CTAGACTCAAATCTGAGGCCAGAGAAGTGTCGTCGCTTTGTCCATCCCCAGTGGCAGCTT 144263
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                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 cttcacctgaatgggactatccacagcacaagtgaggcagaacacagaaccctgtgtggat 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 ctagactcaaatctgaggccagaggagtgtcgtcgctttgtccatccccagtggcagctt 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 ggatctggtaatggaactggaatcctcagtgaagatgccctcttgagaatctctatccca 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 aactttgctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatact 360
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                                                                                            and Chemical Research (RIKEN), Genomic Sciences Center (GSC); kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              totocotttgaacttatotoogtaaagocattgtgcotootottggggggtoaogtgttca 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTCCCTTTGAACTTATCTCCGTAAAGCCATTGTGCCTCCTCTTGGGGGTCACGTGTTCA 143963
                                                                                                                                                                                         Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                1 (bases 1 to 166848)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Tottoki,Y., Wattanabe,H. and Sakaki,Y.
Homo sapiens 166,848 genomic DNA of 11g
published Only in DataBase (2000) In press

2 (bases 1 to 166848)
                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                         Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 11 clone RP11-151E18 map 11q, WORKING DRAFT SEQUENCE, 9 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP002367.1 GI:8131631
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                                        Center: RIKEN Genomic Sciences Center(GSC)
                                               Center code: RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTGS_PHASE1; HTGS_DRAFT.
sapiens DNA, clone:RP11-151E18.
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1 39293 contig of 39293 bp in length
73754 99297 contig of 25544 bp in length
73754 99297 contig of 25544 bp in length
123106 140640 contig of 23608 bp in length
140741 152854 contig of 12114 bp in length
15295 161965 contig of 12114 bp in length
162066 165410 contig of 9011 bp in length
162066 165410 contig of 3345 bp in length
162065 16548 contig of 3345 bp in length
16206 165410 contig of 1338 bp in length
16206 165410 contig of 13758 bp in length
16206 165410 contig of 1386 bp in
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165411 165510: gap of 100 b
165511 166848: contig of 1338
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39394 39393: gap of 100 bp
39394 73653: contig of 34260 bp in length
73654 73753: gap of 100 bp
73754 99297: contig of 25544 bp in length
99398 99397: gap of 100 bp
99398 1323005: contig of 23608 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 6.27x in Q20 bases; sum-of-contigs
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                                                                 140741.
                                                                                                                                                                   /note="assembly_fragment"
123106. .140640
                                                 /note="assembly_fragment"
140741. .152854
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/note="assembly_fragment"
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99398. .123005
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COMMENT

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 161299 CAATCAATGGCCTTTGAGGAGCTCTTGAGTCAAGTTGGAGGCCTTGGGAGATTTCAGATG 161358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 161239 TCTCCCTTTGAACTTATCTCCGTAAAGCCATTGTGCCTCTTTGGGGGTCACGTGTTCA 161298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                               AP000596
                                                                                                                                                                                                                                     ACCESSION
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                                                                                                                                                        ORGANISM
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                                           TITLE
                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 caatcaatggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatg 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 totocotttgaacttatotoogtaaagocattgtgcctcctctttgggggtcacgtgttca 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 cttcacctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtggat 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 ctagactcaaatotgaggccagagaagtgtcgttcgctttgtccatccccagtggcagctt 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 ggatctggtaatgaaactggaatcctcagtgaagatgccctcttgagaaatctctatccca 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 atgagaaattgatgcgaggatcaatacaagcttaatttgaattaataaaaaggaaatattt 120
                                                                                                                                                                                                                                                                                                                                                                                                            541 ggctgggtatatgatcaaagctacttcccttcgaccattgtgactaag 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGATCTGGTAATGAAACTGGAATCCTCAGTGAAGATGCCCTCTTGAGAATCTCTATCCCA 161538
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55669 a 32391 c 31923 g 46064 t
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 116273)

2 (bases 1 to 116273)
                                                                                                                                                                                                                                       ווא טייי, טאר 1 linear HTG 30-MAY-2000 Homo sapiens chromosome 11 clone XXpac-662A14 map 11q13, WORKING DRAFT SEQUENCE, 29 unordered pieces.
APO00596
                                                                                                                                                                                                                    AP000596.2 GI:8118802
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                                                                                                                                                                                                    HTGS_PHASE1;
                                                                                                                                                                           sapiens DNA, clone:XXpac-662A14.
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/note="assembly_fragment clone_end:T7 wector_side:left"
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100.0%; Pred. No. 3.8e-105;
                                                                                                                                                                                                      HTGS_DRAFT
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, pax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-OCT-1999) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: HumDraft11
Center project name: HumDraft11
Center clone name: Xxpac-662A14
Center clone name: Mxpac-662A14
Center clone name: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Chemistry: 1047ap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 103409 bases at least 040
Consensus quality: 11369 bases at least 030
Consensus quality: 11369 bases at least 020
Consensus quality: 11369 bases at least 020
Consensus quality: 13473; sum-of-contigs
Quality coverage: 4.03x in 020 bases; sum-of-contigs
Quality coverage: 4.03x in 020 bases;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 29 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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* arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will

be preserved.

73840 73939: 71388 71487:

73839;

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86778 86877: gap of 100 bp
86878 89783: contig of 2906 bp in length
89784 89883: gap of 100 bp
89884 92751: contig of 2868 bp in length
92752 92851: gap of 100 bp
92852 95068: contig of 2217 bp in length
95069 95168: gap of 100 bp
95169 96739: contig of 1571 bp in length
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96840 97912; contig of 1073 bp in length

97913 98012; gap of 100 bp

98013 99744; contig of 1732 bp in length

99745 99844; gap of 100 bp

99745 99844; gap of 100 bp
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73940 77356; contig of 3427 bp in length
77367 77466; gap of 100 bp
80065; contig of 2599 bp in length
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12467; gap of 100 bp

113665; contig of 1198 bp in length

13765; gap of 100 bp

114974; contig of 1209 bp in length
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                                                            Db 111996 GGATCTGGTAATGAAACTGGAATCCTCAGTGAAGATGCCCTCTTGAGAATCTCTATCCCA 112055
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421 ctagactcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagctt 480
                                                                                                                                                                   301 aactttgctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatact 360
                                                                                   361 ggatctggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatccca 420
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Pred. No. 8.2e-105;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 116273;
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FEATURES

114975 115074: gap of 115075 116273: cont

Location/Qualifiers

112368 112467; gap of 112468

113666 113765:

108530 108629: gap of 108630 110841: cont

104922 105021: gap of

101154 101253: gap of 101254 102868: cont 02869 102968:

101153:

source

misc_feature misc_feature misc_teature misc_feature misc_feature

/note="assembly_fragment" /note="assembly_fragment"

.55534 .60136

/note="assembly_fragment" 44799. .49514

note="assembly_fragment" 18239. .44698 /clone="XXpac-662A14" /map="11q13" /chromosome="11" /organism="Homo sapiens" /db_xref="taxon:9606"

us-09-674-235-19.rge

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Db 112116 CTTCACCTGAATGGGACTATCCACAGCACAAGTGAGGCAGACACAGAGACCCTGTGTGGAT 112175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-FEB-2002) National Institutes of Health, Mammalian Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer General Cancer Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

CDNA Sequencing by: Sequencing Group at the Scanford Human Genome

DNA Sequencing by: Sequencing Group at the Stanford, CA 943

Center, Stanford University School of Medicine, Stanford, CA 943

Center, Stanford, edu

Web site:

Contact: (Dickson, Mark) mcdepaxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_76"
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/db_xref="G1:18490378"
/translation="MARQDLLGHAGDLWREQILQTVELSIEAVATYLHEMLENETAFI
/translation="MARQDLLGHAGDLWREQILQTSNRFEKCRREVHEQWQLLHLN
gedhccwyhildndfvalwodalsodallrisipldsososlfsyakfvemagmavgg
gtfphrsdabmadpcydgwydrisfsstivtemplvcdsososlfsyakfvemagmavgg
gtfphrsdabmadpcydgwydrisfnvpewyciydpgrpgfchsrlayppaggvcTil
IlgghlsdssrvgntqlpghgnvignvpewyciydpgrpgfchsrlayppaggvcTil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 coctttgaacttatctccgtaaagccattgtgcctcctcttgggggtcacgtgttcacaa 183
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                                                                                                                                     TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 catctggtttttattcttccctctctcatgttattaatccctcatatactgctagagaac 303
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                                                                                                                                                                                                                                                                                                                      1986 bp
Sequence 37 from Patent WOO146258.
AX179749
                                                                                                              Baughn, M.R., Burford, N., Au-Young, J., Lu, D.A., Yang, J., Lal, P., Hillman, J.L., Azimzai, Y., Yue, H., Nguyen, D.B., Y Gandhi, A.R., Tang, Y.T. and Khan, F.A.

Transporters and ion channels
Patent: WO 0146258-A 37 28-UUN-2001;
Transporters
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1986)
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                                                                                                       Incyte Genomics, Inc.
              /organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="Incyte ID No: 3358383CB1"
/note="Incyte ID No: 3528 t
3 496 C 457 g 528 t
                                                                                      ocation/Qualifiers
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 Mismatches

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O. Mismatches 150;
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Similarity

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725 GGCATCCTAGGCGGTCATTTATCAGACAGGT 755
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Direct Submission
Submitted (26-MAY-2001) Hitomi Takanaga, Tohoku University,
Graduate Scihool of Pharmaceutical Sciences; Aramaki, Aoba, Sendai,
Aoba-ku, Miyagi 980-8578, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 agaaattgatgogaggatcaatacaagcttaatttgaattaataaaaggaaatattttct 123
                                                                                                                                                            Takanaga,H., Ohtsuki,S., Hosoya,K. and Terasaki,T. Isolation of novel clone of amphiphilic solute facilitator family from human fetal liver
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                            Homo sapiens tissue_lib:fetal liver cDNA to mRNA.
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                       648 tggaatgctggtgggaggcatcataggtggccatgtctcagacaggt 694
                                                                                               588 gtgggacctggtatgtgattatcagtcactgaaatcagtggttcaattcctacttctgac 647
                                                                          503 GTGGGATCTGGTATGTGACTCTCAATCACTGACTTCAGTGGCTAAATTTGTATTCATGGC
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Fax:81-22-217-6886)
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/product="hygn;"
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/product="mappollfhagdlwreqilqtvplsjfavatylhemlenetaej
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PGHRCWVHILDNDTVSDNDTGALSQDALLRISIPLDSNWRPEKCRREVHPGNQLLHHN
ILGGHLSDREGRREVLFWCYLQVAIVGTCAALAPTFLIYCSLRELSGIAAMSLITNTI
ILGGHLSDREGRREVLFWCYLQVAIVGTCAALAPTFLIYCSLRELSGIAAMSLITNTI
SWILESARWLIINNKPEEGLAEUTLAGLAFAIRDWHLIQLVSVPYFVIFITS
KPSLCEMLHMPNICKRISLLSFTRFANFMAYEGLHLHVQHLGNNVFLLQTLEGAVILL
TLAFAHGNEVIPTITGARAMGINATEANLAGILAFILFVQHGTUREVLATLGGASALAN
GCFAFTILDGTBNKBIRGANGINATEANLAGALAPLMMILSYYSPPLPWIIYGFAY
GCFAFTILDGTBNKBIRGTRAFRANGINATEANLAGALAPLMMILSYYSPPLPWIIYGFAY
GCFAFTILDGTBNKBIRGTRAFRANGINATEANLAGALAPLMMILSYYSPPLPWIIYGFAY
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102. .1763
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                                                      TGTGACTCTCAATCACTGACTTCAGTGGCTAAATTTGTATTCATGGCTGGAATGATGTTG
                                                                       tgtgattatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtg
                                                                                                                  TGGGTGTATGACAGAATCTCCTTCTCATCCACCATCGGTGACCTGAAGTGGGATCTGGTA
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Location/Qualifiers
1. 1977
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AX074149
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AP003420/c
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83641 GAGGAAATTGCTTCCGTGACCCTGCTGCAGATGGGAGAGAGGGCCCCATTAAGAAGAGAGT 83582
                                                                                                                                                                                                                                                                                                  83463
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                                                             aaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcacct 488
                                                                                                                                                               tgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatctgg 368
                                                                                                                                                                                                                                                                                                                                                                       GGCCTTTCAGGACCTCCTAGATCAAGTTGGAGGCCTGGGGAGATTCCAGATCCTTCAGAT 83404
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGTCAGGATCAACACACACACTTAGTGTGATTTAAGGAAAGGAAATATTTTCT--CTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCATTCATACTTGATCATCGCTGCTGGGTTCATATACTGGACAATGACACTATCCCTGA 83284
                                                                                                                                                                                                                      GGTTTTCCTTATAATGTTCAACGTCATAGTATACCATCAAACTCAGCTGGAGAACTTCGC
                                                                                                                                                                                                                                          99cctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcatct 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriégsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 160945)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA

Published Only in Database (2001) In press

2 (bases 1 to 160945)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Aug 27, 2001 this sequence version replaced gi:13383333.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-MAR-2001) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete sequence. AP003420
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens genomic DNA, chromosome 11q, clone:RP11-614K12
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31738 c 32047 g 50417
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Pred. No. 6e-57;
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SOURCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacGonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McCheeters, R., Meldrim, J., Meneus, L., Michova, T., Mlenga, V., McPhy, T., Naylor, J., Ngyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Rogov, P., Roman, J., Rosetti, M., Rileback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Strauss, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Straus, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zamhek, I., Zimmer A., and Zodru M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Jones, C., Karatas, A., LaRocque, K., Landers, T.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 11, 2001 this sequence version replaced gi:13270647. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson, B., Wu, X., Wyman, D., Ye, W Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                              Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 157859 bases at least Q40 Consensus quality: 161528 bases at least Q30 Consensus quality: 162934 bases at least Q20 Insert size: 172000; agarose-fp
                                                                                                                                                                                                                                                                                            Center project name: L12735
Center clone name: 3110_P_2
                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                           Sequencing vector: Plasmid; n/a;
                                                                                                                                                                                                                                                                                                                                                              ----- Project Information
Insert size: 163409; sum-of-contigs
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                                                                                                                                                                                                                                                                 Summary Statistics
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41327
57371 57470: gap or
57471 102968: contig
102969 103068: gap of
104809: conti
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12556 15164: contig of 2609 bp in length
15165 15264: gap of 100 bp
15265 16648: contig of 1384 bp in length
16649 16748: gap of 100 bp
16749 29429: contig of 12681 bp in length
29430 29529: gap of 100 bp
29430 29529: gap of 100 bp
29530 41226: contig of 1697 bp in length
41227 41326: gap of 100 bp
41327 57370: contig of 16044 bp in length
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41327. .57370
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'9; gap of 100 bp

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1: gb_ba:*
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Sequence 6 from Patent WO0104283.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtgggatggctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTATATGATCAAAGCTACTTCCCTTCGACCATTGTGACTAAGTGGGACCTGGTATGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAAATCTGAGGCCAGAGAAGTGTCGTCGCTTTGTCCATCCCCAGTGGCAGCTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tcaaatctgaggccagagaagtgtcgttcgtttgtccatccccagtggcagcttcttcac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTAATGAAACTGGAATCCTCAGTGAAGATGCCCTCTTGAGAATCTCTATCCCACTAGAC 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGCAGCCATTCCTGGTCATCGTTGCTGGGTCCACATGCTGGACAATAATACTGGATCT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gctgcagccattcctggtcatcgttgctgggtccacatgctggaccaataatactggatct 180
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                                                                                 (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Aug 27, 2001 this sequence version replaced gi:13383333.
                                                                                                                                                       Submitted (16-MAR-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             508;
                                                                                                                                                                                                                                   1 (bases 1 to 160945)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA published Only in Database (2001) In press
2 (bases 1 to 160945)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens genomic DNA, chromosome 11q, clone:RP11-614K12,
                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                          .160945
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Pred. No. 2.4e-136;
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JOURNAL REFERENCE
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AP002367
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                                                                                                                                                                                                                     and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Only in DataBase (2000) In press 2 (Dases 1 to 166848)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yadd,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 166,848 genomic DNA of 11q
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                             Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                                                                                        Center code: RIKEN
                                                                                                                                              Center: RIKEN Genomic Sciences Center(GSC)
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Project Information
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Pred No. 1.5e-105;
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140741 152854 contig of 17535 bp in length
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152956 165410 contig of 9011 bp in length
165215 166848 contig of 3345 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Chemistry: 162010 bases at least Q40 Consensus quality: 162010 bases at least Q30 Consensus quality: 164639 bases at least Q30 Consensus quality: 165230 bases at least Q20 Insert size: 166048; sum-of-contigs Quality coverage: 6.27x in Q20 bases; sum-of-contigs Quality coverage: 6.27x in Q20 bases;
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123106 14064(
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140741 152854: cont
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165511 166848: cont
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162066 165410: conti
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73754. .99297
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152955. .161965
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                                                                               140741. .152854
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140640: cc
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Local Similarity 100.0%; Pred. No. 1.5e-105;
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                                                                                                                                                                                                                                                                                                                                                  Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yadd,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA published Only in DataBase (2000) In press published 1 to 16976)

2 (bases 1 to 16976)

2 (bases 1 to 16976)

3 (bases 1 to 16976)

5 (bases 1, Vada,T., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.,
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                                                                                                                                                     Submitted (24-APR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Yokohama, Kanagawa 230.0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230.0045, Japan 1-7-22 Suehiro
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165511. 166848
/note="assembly_fragment"
132391 c 31923 g 46064 t 801 others
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162066. .165410
                                                                , 2001 this sequence version replaced gi:10716820. Location/Qualifiers
1. .169776
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/db_xref="taxon:9606"
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/chromosome="11"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61697 CTGGTTTTTATTCTTCCCTCTCTCATGTTATTAATCCCTCATATACTGCTAGAGAACTTT 61756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 gtatatgatcaaagctacttcccttcgaccattgtgactaag 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtggatggctgg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ctggtttttattottcoctctctcatgttattaatccctcatatactgctagagaacttt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 atggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcat 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                Center project Information
Center project name: H_NH0204K20
Summary Statistics
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
                                                                                                                                                                                 MO 63108, US
On Jun 16, 2
                                                                                                                                                                                           Direct Submission
Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                              Waterston, R.H.
                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                  The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                           Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                           ------ Genome Center -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC073256 170682 bp DNA linear HTG 07-JUL-2000 HOMO Sapiens chromosome 11 clone RP11-204K20, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AC073256.2 GI:8569847
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                                                                                                                                                              2000 this sequence version replaced gi:8468975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%; Score 402; DB 9; L6 100.0%; Pred. No. 1.5e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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misc_feature
                          misc_feature
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* NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 157404 bases at least Q40 Consensus quality: 160944 bases at least Q30 Consensus quality: 160944 bases quality: 160944 bases quality: 160944 bases quality: 160944 bases quality: 160944 bas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 4.52 in Q20 bases; agarose-fp Quality coverage: 4.50 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 161000; agarose-fp
Insert size: 168782; sum-of-contigs
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127051
127151
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19999
24951
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11646
15817
/note="assembly_name:Contig12" 6731. .11545
                                                                             /note="assembly_name:Contig11"
                                                                                                                                                                                                              /note="assembly_name:Contig9" 2301. .3481
                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
                                                                                                                                               /note="assembly_name:Contig10
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .17068
                                                                                                                                                                                                                                                                                                       /clone="RP11-204K20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82742: gap of unknown length
94996: contig of 12254 bp in length
95096: gap of unknown length
108127: contig of 13031 bp in length
127050: contig of 18823 bp in length
127150: gap of unknown length
127150: gap of unknown length
127150: gap of unknown length
144499: contig of 17349 bp in length
144599: gap of unknown length
144599: gap of unknown length
14659: gap of unknown length
170682: contig of 26083 bp in length
                                                                                                                                                                                                                                                                                 . 2200
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2300: gap of unknown length
3481: contig of 1181 bp in length
4832: gap of unknown length
4832: contig of 1251 bp in length
4932: gap of unknown length
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gap of unknown leng
contig of 4815 bp 1
gap of unknown leng
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contig of 3982 bp in length
gap of unknown length
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lg of 5299 bp in length
f unknown length
length
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lg of 4952 bp in length
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25686 TCAAATCTGAGGCCAGAGAAGTGTCGTCGCTTTGTCCATCCCCAGTGGCAGCTTCTTCAC
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                                                                                                        361 gtatatgatcaaagctacttcccttcgaccattgtgactaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ctggtttttattcttccctctctcatgttattaatccctcatatactgctagagaacttt 120
                                                                                                                                                                                                                  ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtgggatggctgg
                                                                                                                                                                                                                                                                                                      tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac
                                                                                                                                                                                                                                                                                                                                                                     GGTAATGAAACTGGAATCCTCAGTGAAGATGCCCTCTTGAGAATCTCTATCCCACTAGAC
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144600, 170682
/note="assembly_name:Contig28"
33360 c 33713 g 50161 t
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43294. .52430
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11646. .15816
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19999. .24950
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127151. .144499
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72574. .82642
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  HTG 30-MAY-2000
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, Tel:81-42-778-9923, Fax:81-42-778-9924)
On May 31, 2000 this sequence version replaced gi:6997486.
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Submitted (12-OCT-1999) Masahira Hattori, The Institute of Physical
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Center project name: HumDraftil
Center clone name: XXpac-662A14
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Contact: hattori@gsc.riken.go.jp
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16 runs of N, but the exact sizes of the gaps are unknown.
17 This record will be updated with the finished sequence
18 as soon as it is available and the accession number will
18 be preserved.
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66 80165: gap of 100 bp in 10
66 83825: contig of 3660 bp in 10
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70102: contig of 4379 bp in
70202: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 37 Row: d Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1566)
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Tissue Procurement: CLONTECH
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    CDLSDLKLAARVCSVAHYQQ"
375 c 356 g
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/tissue_type="Liver"
/clone_lib="NIH_MGC_76"
/lab_host="DH10B"
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/protein_id-"AAH22379.1"
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M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ∕organism≔"Homo sapiens"
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                                                                                                                Graduate School of Pharmaceutical Sciences; Aramaki, Aoba, Aoba-ku, Miyagi 980-8578, Japan (E-mail:takanaraamaki)
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens ust3 mRNA for hUST3, ABD62418
                                                                                                                                                                                                                                                      Takanaga, H., Ohtsuki, S., Hosoya, K. and Terasaki, T. Isolation of novel clone of amphiphilic solute facilitator
                                                                                               Fax:81-22-217-6886
                                                                                                                                                                            Direct Submission
                                                                                                                                                                                          Takanaga, H.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                              E-mail:takanaga@mail.pharm.tohoku.ac.jp,
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/tissue_lib="fetal liver" 102. .1763
                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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AX179749
AX179749.1
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Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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// Geno_start=1
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SWLLESARWLIINNKPEGGLKELRKAAHRSGMKNARDFILTEILKSTMKKELEAAOKK
KPSLCEMLHMPWICKRISLLSETREANETMAYEGLHYOHLGNUVETLOTLFGAVILL
ANCVAPWALKYMNRRASOMLLHEILAICILAIITVPQEMOTLREVLATIGIGASALAN
TLAFAHGNEVIPTIRARAMGINATFANIAGALAPLMMILSVYSPPLPWIIYGVFPFI
SGFAFILLPGTRNKPLPDTIQDEXNERKDPREPKQEDPRVEVTQF"
158 a 472 c 420 g 496 t
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37 from Patent W00146258
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Craniata; Vertebrata; Catarrhini; Hominidae,
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   Hominidae;
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                 Euteleostomi;
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                                         Sun, W.
                                                                                                                                                               Sequence 5 from Patent W00104283
              Patent:
                            Organic
                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                     Homo sapiens
Metabasis Therapeutics
                                                                                                                                                    AX074149.1
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Baughn,M.R., Burford,N., Au-Young,J., Lu,D.A.,
Lal,P., Hillman,J.L., Azimzai,Y., Yue,H., Nguye
Gandhi,A.R., Tang,Y.T. and Khan,F.A.
Transporters and ion channels
Patent: WO 0146258-A 37 28-JUN-2001;
Incyte Genomics, Inc. (US)
    Location/Qualifiers
    1. .1986
                                                          (bases 1 to 1977)
           anion transporter genes and WO 0104283-A 5 18-JAN-2001;
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/db_xref="taxon:9606"
/note="Incyte ID No: 3358383CB1"
/ 496 c 457 g 528 t
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Pred. No. 3.4e-86;
0; Mismatches 108;
                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                          TITLE
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                                         AUTHORS
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395; Conserv
                                                                             Molecular cloning and characterization proteins from rat kidney FEBS Lett. 425 (1), 79-86 (1998)
      Direct Submission Submitted (10-DEC-1996) D.
                                                                                                                                       1 (bases 1 to 2597) Schomig, E., Spitzenberger, F., Engelhardt, M., Martel, F., Ording, N.
                                       Gruendemann,D.
                                                                                                                                and Grundemann, D.
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                               Norway rat.
                                                                                                                                                                                                                                                       integral membrane transport protein; UST1r gene
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Y09945
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/db_xref="taxon:9606"
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1. .1977
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Pred. No. 4.
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    Gruendemann,
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Local Similarity 74.48;
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                                                                       TOTCAGTCACTGGATTCAATAGCTAAGTTTCTATTCTTGACTGGTATCTTAGTAGGAAAT
                                                                                                                                                                                                                                                                                                                                                                                               ATCCTATATGGCCCCTTAACAGACAGGT 594
                                                                                              tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtggggggg 480
                                                                                                                                                        GTGTATGACCAAAGCACCTTTCTTTCCACCATTATTACCGAGTGGGACCTGGTGTGAA
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87. 17.
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SALVHANELLFTIIRATALGVIGIAGSTGAALSPLFMILRTYSDSLPWIIYGVLSFLG
GLVVLLLPETKNGPLPDSIQDVENEGRASRQGKQNDTLIKVTQF"
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/protein_id="CAA71076.1"
/db_xref="GI:3004482"
/db_xref="SPTREMBL:070609"
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87. .1745
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Pred. No. 5.6e-76;
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tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac
                                                          GATAATAACAGTAGGATCCTGAGCCAAGATGACCTCCTAAGGATCTCCATCCCAATGGAC
                                                                              ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
                                                                                                                                                                  gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                                                                                                                                             TTGATTTTTGTACTGATCTGCTTTATCCTGGTAGTTCCTCACACTGTTTTGGAGAACTTC
                                                                                                                                                                                                                                               ctggtttttattcttccctctctcatgttattaatccctcatatactgctagagaacttt 120
                                                                                                                                                                                                                                                                                      ATGGCCTTTCAGGACCTTATAACTCAAATTGGCTGCCTGGGGAGGTTCCAGATCCTTCAC 180
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                                                                                                                                                                                                                                                                                                                                                              374;
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422 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-NOV-2000) Seok Ho Cha, Kyorin University School Medicine, Department of Pharmacolgy and Toxicology; 6-20-2 Shinkawa, Mitaka, Tokyo 181-8611, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cha, S., Sekine, T., Ono, T., Hasegawa, M., Kanai, Y. and Endou, H. Molecular cloning and characterization of multispecific organic anion transporter 5 expressed in the kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (strain:Sprague-Dawley) cDNA to clone_lib:rat kidney cDNA library clone:rOAT5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus mRNA for organic anion transporter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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LLILEMTSPKFQAMVMALIESAGGIGGVLGVLAFGIRNWCHLOLAMSVPVFFFLLIFT
RWLSESARWLIITNKPOEGLKELIKVAHINGIKSRDVLTEVVKTTMKDELEÄAETK
PSPLYLFRTPMLRKRICLLSFVRCVSLISTVGLLINLOYLSNKVFLLOCKJGVCTPA
NLLGNFSMNYMGRRTTGIIFMSVMGISJLSITFLTQEMQIPRLVLASLGGAISSASLT
STAVLSNELVPTVIRATALGVIGIFGSAGAALSPLLMILMTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MAFQDLITQIGCLGREQILHLIFVLICFILVVPHTVLENFTAAI
PSHRCWVPILDNUTMSDNNSRILSQDDLLRISIPMDSNLRPEKCRRYIQPQWDLLHLN
GTFSTVTEPDTEPCVDGWVYDQSTFLSTTVTQWDLVCGSQTLNSVAKFIYMTGIFIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLVVLLLPETRNQPLPDSIQDVENKRKSSREVKKDAVAKVTPF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="organic anion transporter 5"
/protein_id="BAB78471.1"
/db_xref="GI:17221620"
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121. .1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="rOAT5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 2253)
                                                                                /db_xref="taxon:9606"
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         /codon_start=1
                           /note="unnamed protein product"
                                                                                                                                                          /organism="Homo sapiens"
                                                                /note="cloning vector:
                                               .1866
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481 atcataggtggccatgtctcagacaggt 508
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Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Momura,R.,
Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H.,
Yongawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E.,
Kataoka,R., Kuga,N., Kuroda,A., Satoh,I., Kamata,K., Takahashi,E.,
Terrashima,Y., Watanabe,M., Sugiyama,T., Irie,R., Otsuki,T.,
Sato,H., Ota,T., Wakamatsu,A., Ishi,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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                                                                                                                      Submitted (24-007-2001) Takao Isogai, Helix Research Institute, Submitted (24-007-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951) Fax:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-6 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and HRI, and Biotechnology Center, National Institute of Technology and
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                                                                                Evaluation; clone selection for full insert sequencing: RAB and
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                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 atcataggtggccatgtctcagacaggt 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               688 ATCATATGTGGCCATTTGTCAGACAGGT 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 TCCAACCTGAGACTGGATAAATGTCGTCGTTTTGCCCAACCACAGTGGCATCTTCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 ATCTCTTTGTTCTCTCCTCGTAGGCCTTGTGGTACCTCATATTACAATGGAGAACTTT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTCAGGCACTGAATTCTGTTGCTAAATTTTCATTCATGATTGGCCTATTTATAGGGGCT 687
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Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                    Strausberg,R
                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC021384.1 GI:18204002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus, clone MGC:29260 IMAGE:5064542, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                               nouse mouse
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SSPRDLFHTPILRKRICVLSFMRYLFTISIFGLSLHLQHLSTNIILLQFLSSALGILI
SVIGHTVLNHMGRRITQLVLMSLRGIFMLTAVFVPQEMQTLRIIMATLAAALSSLCMC
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/db_xref="GI:16553417"
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73.6%;
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Pred. No. 4.1e-74;
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                                                                                                                                                                                                                                   Murinae; Mus
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181 ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
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                                                                                                                                                                                                                       144 ATGATATTTGTGTTAATCTGCCATGCCCTGTCGGCTCCTCACACTCTTTTGGAGAACTTC 203
                                                                                                                                                                                                                                                                           61 ctggtttttattcttccctctcatgttattaatccctcatatactgctagagaacttt 120
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                                                                                                                                gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                             ACTGCAGCCATTCCTAGTCATCGCTGCTGGGTCCCCATCCTTGACAATGACACTGCCTCT
                                                                                                                                                                                                                                                                                                                                               ATGGCCTTTCAGGACCTTATAATTCAAATTGGCAGCTTGGGGAGGTTCCAGATTCTTCAC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 39 Row: n Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: nisc_mgc@nhgri.nih.góv
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Legaspi,R.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduco,Q.L., Masiello,C., Mastrian,S.D., McCLoskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
McDowell,J., Pearson,R., Snyder,B., Stantripop, S., Thomas,P.J.,
Thongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaithersburg, Maryland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Jeffrey E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSHRCWYPILONDTASDNGSRILSQDDLLRISIPLDSNLRPDKCRRYIQPQWHLLHLN
GTFPTYTEPDTEPCYDGWYZDGSTFLSTTYTQWDLVCGSQALMSVAKFIYMTGIFIGY
IMGGHLSDKFGRKLIFTCSLLKMAITTETCVAFADSFLIYGSLRFLSGIFSSTLRTNSA
LLILEWTSPKRQALVMALIFIASGVGQTLLGGLAFAFRNWHHLOLALSYPMFLLLIFT
RWLSESARWLIMANKPQKSLKELKKAACVNRIKNSGDALTLEVVKTIMKEELEAAQTK
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NVLGNFSMNYMGRRMTQLIFMSVLGISILAVVFLPQEMQILRVFLSTLGGAISSASIT
STLVHANELVFTIIRATALGVVGIAGSAGGALSPLLMILTTYSASLPWIIYGILPFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLVALLLPETKNQPLPDSIQDIENKRKSSKEAKKDVVAKVTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Unknown (protein for MGC:29260)"
/protein_id="AAH21384.1"
/db_xref="GI:18204003"
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84. .1739
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/clone_lib="NCI_CGAP_Kid14"
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/clone="MGC:29260 IMAGE:5064542"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                              //product=Putative integral membrane transport protein /protein_id="CAC79639_1"
//b_xref="GI:18076049"
//db_xref="GI:18076049"
//translation="MARGELLKQVGGLGRFQILQMVFVVFTSVIVVPHIIIENFTAAI /translation="MARGELLKQVGGLGRFQILQMVFVVFTSVIVVPHIIIENFTAAI PSHRCWYPILDNUTYSDNDSRILNQDKLLKISIPEDDSHLEDKCRFFAQPQWHLLDLN PSHRCWYPILDNUTYSDNDSRITSTCAGFAPNLFIYCSLRFLAGMSLEPITVNIN DIFSLIEDFECKFILKYALLQMAITETCAGFAPNLFIYCSCARFEAGMSLEPITVNIN LLMFEWTSFKFLTMYTVLGSCAGSFGGMILAGLAFQFOMHHLQLAMSVPIFFFLILT RWLPESARWLIVINKPOKGLKELKVAAHINGMKKSGDNITMEVVRTSMKKELEAAKMR PSPROLFHTPILRKQIYILSFIRLFILSGVGVAHLQHLSNNLELLQILISVSSILF SVIGHEVLNHIGRRITOMVIMFLRGISILTALFARQEMETLRFIMAMAEGLAALSYA ANSLHANELLPTILRATARGVIGMEGNIGFFPAPLCMMLVSYSPLDWHIFYGGFAILS GFIVLLLPETKNNPLDDCTHDVENDWESSRQEMKEDPIIKVTRF"
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121. .1779
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/db_xref="taxon:10116"
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121. .1779
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             atcataggtggccatgtctcagacaggt 508
                                                TCTCAGGCACTGAATTCTGCCACTAAACTTTCATTTATGATTGGTGCATTTATAGGAGGT
                                                                        tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc 480
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Search completed: July 1, 2002, 15:41:50 Job time: 10924 sec

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Q96DT2;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ORGANIC ANION TRANSPOTER 4 LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "human organic anion transporter 4 similer gene."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB050269; BAB68364.1; ". SEQUENCE 552 AA; 58729 MW; BE2A3EA23B98B420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-KIDNEY SPECIFIC;
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                                                                                                                                           229 RPLYMTLNSLGFSFGHGLTAAVAYGVRDWTLLQLVVSVPFFLCFLYSWWLAESARWLLTT 288
                                                                                                                                                                                                                                                                                          109 ARPTRSRVWMAGSMTAASSPPQSWQVELVCDSHALKPMAQSIYLAGILVGAAACGPASDR 168
                                                                                                                                                                                                                                                                                                                              113 TEPCVDG-WVYDQSYFPSTIVTKW--DLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR 169
                                                                   289 GRIDWGIQELWRVAAINGKGAVQDTLTPEVILSAMREELSMGQPPASIGTLIRMPGIRFR 348
                                                                                                      182 NKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKR 241
                                                                                                                                                                                                                    169 FGRRLVLTWSYLQMAVMGTAAAFAPAFPVYCLFRFLLAFAVAGVMMNTGTLLMEWTAARA 228
 349 TCI 351
                                242 ICI 244
                                                                                                                                                                                                                                                                                                                                                                   61 ASILGSLSPEALLAISIPPGPNQSP-----ISAAASASHSGSSWTPMPRPPAG 108
                                                                                                                                                                                                                                                                                                                                                                                        1 MAFSELLDLYGGLGRFQYLQTMALMYSIMWLCTQSMLENFSAAVPSHRCWAPLLDNSTAQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97; Indels 131; Gaps
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Search completed: July 1, 2002, 11:42:46 Job time: 216 sec

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RESULT 13
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 Nigam S.K.;

"Molecular cloning and characterization of NKT, a gene product related to the organic cation transporter family that is almost exclusively expressed in the kidney.";

J. Biol. Chem. 272:6471-6478(1997).

J. Biol. Chem. 272:6471-6478(1997).
                                                                                                                                                                                                                              Q61185 PRELIMINARY; PRT; 545 AA.
Q61185; Q61185; Q61185;
Q1-NOV-1996 (TremBLrel. 01, Created)
Q1-NOV-1996 (TremBLrel. 01, Last sequence update)
Q1-DEC-2001 (TremBLrel. 19, Last annotation update)
KIDNEY-SPECIFIC TRANSPORT PROTEIN.
J. Biol. Chem. 272:6471-6478(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                        MEDLINE-97197822; PubMed-9045672;
Lopez-Nieto C.E., You G., Bush K.T., Barros E.J.,
                                                                                                                           STRAIN-BALB/C;
                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -EPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR--- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADT----- 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPFSELLEQVGSTGRFQVLHVTLLCIPVLMMASHNLLQNFVATVPSHYCNAH-----AN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
7LINKED (GLCNAC. . .) (POTENTIAL);
7DC1A67F32801D2D CRC64;
                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                           Beier D.R.,
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                                                                                                                                                                                Murinae; Mus
                                                              product related
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          Q96TC1 PRELIMINARY; PRT; 542 AA.
Q96TC1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                              Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB042505; BAB47393.1; -.
                                                                                                                                                                                                                                        Cha S., Sekine T., Kanai Y., Endou H.; "Molecular cloning and characterization of human organic transporter 3.";
                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U52842; AAC53112.1; -. MGD; MGI:892001; S1c22a6. InterPro; IPR003662; sub_transporter. Pfam; PF00083; sugar_tr; 1.
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    61 V----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 YSLGQFLLAGIAYAVPHWRHLQLAVSVPFFVAFIYSWFFIESARWYSSSGRLDLTLRALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 LQTAVSGTCAAYAPNYTVYCIFRLLSGMSLASIAINCMTLNMEWMPIHTRAYVGTLIGYV 223
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                          VHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSE 110
                                                        MTFSEILDRVGSMGHFQFLHVAILGLPILNMANHNLLQIFTAATPVHHCRPPHNASTGPW
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                                                                                                                                      Similarity
                                                                                                                                                                                                542 AA;
                                                                                                                        Conservative
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                                                                                                                                   27.8%;
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28.7%; Pred. No. 5.8e-34;
29. Mismatches 77;
                                                                                                                      46;
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                                                                                                                                 Score 390.5; DB 4
Pred. No. 2.6e-29;
--LPMGPNGKPERCLRFVHPP----NASLPNDTQ
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RESULT
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                                   Q9TSY7 PRELIMINARY; PRT; 551 AA.
Q9TSY7;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RENAL ORGANIC ANION TRANSPORTER 1 (RBOAT1).
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TRANSMEM
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TRANSMEM
     Eukaryota;
                Oryctolagus
                            ROAT1.
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J. Biol. Chem. 272:18526-1
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                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE SLC22 FAMILY OF TRANSPORTERS L; AF008221; AAC18772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 272:18526-18529(1997).

FUNCTION: MEDIATES THE NA(+)-INDEPENDENT TRANSPORT OF ORGANIC ANIONS SUCH AS CYCLIC NUCLEOTIDES, PROSTAGLANDIN E2 AND URIC & SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL MEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: STRONG EXPRESSION IN KIDNEY. VERY WEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKELETAL MUSCLE, SMALL INTESTINE, LARGE INTESTINE, EXPRESSED IN THE PROXIMAL TUBULE IN THE KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXPRESSION IN BRAIN.
                                                                                                                                                                                     KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFL
                                                                                                                                                                                                                                                                                                            VYDNSTFPSTIVTEWNLVCSHRAFRQLAQSLYMVGVLLGAMVFGYLADRLGRRKVLILNY 169
                                                                                                                                                                                                                                                                                                                                       VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR-------
                                                                                                                                                                                                                                                                                                                                                              AN----LSKDGGLEAWLPLDKQGQPESCLRFTSPQWGPPFYNGT-EANGTRVTEPCIDGW 109
                                                                                                                                                                                                                                                                                                                                                                                      GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                             YSLGQFLLAGIAYAVPHWRHLQLVVSVPFFIAFIYSWFFIESARWYSSSGRLDLTLRALQ
                                                                                                                                                                                                                                                              LQTAVSGTCAAYAPNYTVYCVFRLLSGMSLASIAINCMTLNVEWMPIHTRAYVGTLIGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pro; IPR003662; sub_transporter.
PF00083; sugar_tr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYCOSYLATED (BY SIMILARITY)
   Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
338
396
485
39
56
92
97
               cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
216
269
358
416
505
505
56
92
113
   Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60766 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOT DETECTED IN HEART,
LL INTESTINE, LARGE INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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N-LINKED (GLCNAC.
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N-BBA47BE628324BF2 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 457.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                                                                   -----VESARWLIITNKLDEGLKALR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.5e-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EYE OR TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               119;
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                                                                                                                                                               345
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                  057379;
                +
                                                                                         "Expression cloning and characterization transporter from winter flounder."; FEBS Lett. 417:287-291(1997).
                                                                                                                                                                                                                                                    Pseudopleuronecta americanus (Winter flounder).

Pseudopleuronecta americanus (Winter flounder).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom

Actinopterygii, Neopterygii; Teleostei, Euteleostei; Neoteleost

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Carea 01-JUN-1998 (TrEMBLrel. 10, Last 01-JUN-2001 (TrEMBLrel. 17, Last RENAL ORGANIC ANION TRANSFORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bahn A., Knabe M., Hillemann A., Burckhardt G.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY
                                                                                                                                                                             TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: INTEGRAL ME-!- SIMILARITY: BELONGS TO THE SUGAR EMBL; AJ242871; CAB62587.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=KIDNEY CORTEX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9986;
                                                                                                                                          Wolff N.A., Werner A., Burkhardt S., Burckhardt G.;
                                                                                                                                                           MEDLINE=98072393; PubMed=9409735;
                                                                                                                                                                                       SEQUENCE FROM N.A., AND FUNCTION
                                                                                                                                                                                                                                         Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00083; sugar_tr;
                                                                                                                                                                                                                        NCBI_TaxID=8265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                            ANIONS SUCH AS P-AMINOHIPPURATE SUBCELLULAR LOCATION: INTEGRAL 1
                                 MEMBRANE (POTENTIAL).
                                                                               FUNCTION: MEDIATES THE NA(+)-INDEPENDENT TRANSPORT OF ORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVARINGKQEEGAKLSMEVLRTNLQKELTMSKGQASAMELLRCPALRHLFLCLSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YSTGQFLLAGVAYAVPHWRYLQLLVSVPFFAFFVYSWFFIESARWYSTPGRLDLTLKALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQTAVSGTCAAFSPNFTVYCTFRLLSGMSLAGIALNCMTLNVEWMPIHTRAYVGTLAGYV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYDNSTFPSTIVTEWDLVCSHRALRQLGQSLYMAGVLIGAMVFGYLADRLGRRKVLILNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAFNDLLKQVGGVGRFQRIQVTLVVLPLLLMASHNTLQNFTAAIPPHHCRPPAHAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LSKDGGLQAWLPQDTQGRPKSCLRFTSPQERPPFLNGT-EANGTGTTEPCTDGW 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105;
                GLYCOSYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003662; sub_transporter.
                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA; 60588 MW;
 BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.0%;
             (BY SIMILARITY)
TO
THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                  Last annotation
                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 449.5; DB (
Pred. No. 5.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
SLC21 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69C25F96B154517E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                               MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                   562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSPORTER FAMILY
                                                                                                                                                                                                                                                                       Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                     Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                            of a renal organic anion
OF TRANSPORTERS
                                               PROTEIN.
                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -VESARWLIITNKLDEGLKALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 119;
                                                 BASOLATERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289
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transporter gene (hoatl).";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: MEDIATES THE NA(+)-INDEPENDENT TRANSPORT OF ORGANIC ANIONS SUCH AS P-AMINOHIPPURATE AND ALPHA-KETOGLUTARATE.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99160894; PubMed=10049739; Race J.E., Grassl S.M., Williams W.J., Holtzman E.J.; Race J.E., Grassl S.M., Williams W.J., Holtzman E.J.; "Molecular cloning and characterization of two novel human renal organic anion transporters (hOATI and hOAT3)."; Biochem. Biophys. Res. Commun. 255:508-514(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bahn A., Prawitt D., Reid G., Enklaar T., Wolff N.A., Hillemann A., Godehardt S., Buttler D., Knabe M., Schulten H.J., Gunawan B., Fuezesi L., Zabel B., Burckhardt G.; "Genomic cloning and characterization of the human renal organic anion "Genomic cloning".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lu R., Chan B.S., Schuster V.L.; "Cloning of the human Kidney Protein kinase C."; specificity and regulation by protein kinase C."; hm. J. Physiol. 276:F295-F303(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reid G., Wolff N.A., Dautzenberg F.M., Burckhardt G.; "Cloning of a human renal p-aminohippurate transporter, Kidney Blood Press. Res. 21:233-237(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-98433806; PubMed-9762842;
Reid G., Wolff N.A., Dautzenberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hosoyamada M., Sekine T., Kanai Y., Endou H.; o "Molecular cloning and functional expression o organic anion transporter from human kidney."; hm. J. Physiol. 276:F122-F128(1999).
                              Pfam; PF00083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The antiviral nucleotide analogs cidofovir and adefovir are novel substrates for human and rat renal organic anion transporter 1."; Mol. Pharmacol. 56:570-580(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sweet D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cihlar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99137667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=KIDNEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99103997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99393620; PubMed=10462545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.
                                                        MEMBRANE (POTENTIAL).

ALTERNATIVE PRODUCTS: 2 ISOFORMS; ISOFORM HOAT1-1 (SHOWN HERE)
AND ISOFORM HOAT1-2; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: STRONGLY EXPRESSED IN KIDNEY. ALSO DETECTED
BRAIN AND AT LOW LEVELS, IN SKELETAL MUSCLE AND PLACENTA. NOT
EXPRESSED IN HEART, LUNG, LIVER, PANCREAS, COLON, THYMUS, SMALL
INTESTINE OR PERIPHERAL BLOOD LEUKOCYTES. IN THE KIDNEY, STRONGLE
EXPRESSED IN PROXIMAL TUBULE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T., Lin D.C., Pritchard J.B., Fuller M.D., Mendel D.B.,
                              IPR003662; sub_transporter.
)083; sugar_tr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
              Transport; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9887087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=9950961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION
                                                                                                                                                                                    SLC22 FAMILY OF TRANSPORTERS
            splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a multispecific
              Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hROAT1.";
                                                                                                                                                                                                                                     STRONGLY
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RESULT
035956
ID 03
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Best Local Similarity
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035956;

01-JAN-1998 (TrEMBLrel. 0

01-JAN-1998 (TrEMBLrel. 0

01-JUN-2001 (TrEMBLrel. 0

01-JUN-2001 (TrEMBLrel. 0
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RENAL ORGANIC ANION TRANSPORT PROTEIN 1.
                                                         Sweet D.H., Wolff N.A., Pritchard J.B.; "Expression cloning and characterization o organic anion transporter in rat kidney."; J. Biol. Chem. 272:30088-30095(1997).
MEDLINE=97373539; PubMed=9228014; Sekine T., Watanabe N., Hosoyamad
                       SEQUENCE FROM N.A., FUI
STRAIN-SPRAGUE-DAWLEY;
                                                                                                          MEDLINE-98043701;
                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                         SLC22A6 OR ROAT1
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                                                                                                                      TISSUE=KIDNEY;
                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                           Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFL
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39
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92
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                                                                                                          PubMed=9374486;
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Rodentia;
                                  FUNCTION,
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                        TISSUE-KIDNEY;
  Hosoyamada
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N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT

MISSING (IN ISOFORM OAT1.2)

G -> S (IN REF. 3).

L -> F (IN REF. 2).

MY: 74AD3EA2678032E4 CRC64;
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                                    AND TISSUE
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                                    SPECIFICITY
                                                                                   of ROAT1. The
                                                                                                                                 SPECIFICITY
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                                                                                                                                                                       Murinae;
                                                                                   basolateral
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                                                                                                                                                                       Rattus
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PRELIMINARY; PRT; 506 AA. 00 (Tremblrel 15, Created) 00 (Tremblrel 15, Last sequence upon (Tremblrel 19, Last annotation NETY (NoAT) pubmed-10964714; Trawitt D. Buttler D., Reid G., Enk C., Hillemann A., Schulten H.J., Gency (Tremblys. Res. Commun. 275:623-630(20) LULAR LOCATION: INTEGRAL MEMBRANE property (Tremblys. To THE SUGAR TRANSPORTY (Tremblys. To THE SUGAR TRANSPORTY (Tremble 29, 28; Debase (Tremble 29, 28; Debase (Tremble 29, 28; Debase (Tremble 29, 28; Pred No. 6.1e-38; Conservative 51; Mismatches (Trembly (Trembl	OPNOC2 ID OPNOC2 AC OPNOC2: AC OPNOC2: DT O1-OCT-2000 (TrEMBLrel. 15, Created O1-DCT-2000 (TrEMBLrel. 15, Last see O1-DEC-2001 (TrEMBLrel. 15, Last see OT O1-DEC-2001 (TrEMBLrel. 19, Last ann GN OAT1. GN OAT1. CO HOMO SAPIENS (HUMAN). CE LEWARYOTA; METAZOA; CHOTDATA; CTANIS PORTER. OS HOMO SAPIENS (HUMAN). CE LEWARYOTA; METAZOA; CHOTDATA; CTANIS PORTER. OX NCBL_TAXID-9606; RN GIJ_TAXID-9606; RN SEQUENCE FROM N.A. RC TISSUE-KINNEY; RX MEDLINE-20422308; PubMed=10964714; RA BANN A., PRAWITT D., Buttler D., Rel Ebbinghaus C., Hillemann A., Schulte RA Ebbinghaus	121 VYDGSYE 121 VYDHSTH 170 181 LLVSVSG 170 241 FSFGQVL 193 KVARTNG 193 KVARTNG 191 RVAAVNR
update) on update) charata; Euteleostomi; Hominidae; Homo. Enklaar T., Wolff N.A., Gunawan B., Fuezesi L., of the human organic anion (2000). E PROTEIN (BY SIMILARITY). PORTER FAMILY. E6C5E CRC64; B2; Indels 119; Gaps 82; Indels 119; Gaps 82; Indels 119; Gaps ENFAAAIPGHRCWVHMLDNNTGS 60 2NFTAAIPTHHCRPPAD 54 LLHLNGTIHSTSADTEPCVDGW 120 1	sequence update) sequence update) annotation update) annotation update) niata; Vertebrata; Euteleostomi; niata; Vertebrata; Homo. niata; Vertebrata; Euteleostomi; arrhini; Hominidae; Homo. Redd G., Enklaar T., Wolff N.A., Iten H.J., Gunawan B., Fuezesi L pression of the human organic an 5:623-630(2000). L MEMBRANE PROTEIN (BY SIMILARIT JAR TRANSPORTER FAMILY. SEAS 5: DB 4; Length 506; NO. 6.1e-36; NO. 6.1e-36; SMATCHES 82; Indels 119; Ga ELIPHILLENFAAAIPGHRCWVHMIDNNTGS : LMASHNTLQNFTAAIPTHC	VYDQSYEPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR

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Best Local Similarity
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                                                          O95742 PRELIMINARY; PRT; 563 AA.
O95742; O95187; O9UBC08; O9UBC6;
O1-MAY-1999 (TremBLrel. 10, Created)
O1-MAY-1999 (TremBLrel. 10, Last sequence update)
O1-JUN-2001 (TremBLrel. 17, Last annotation update)
RENAL ORGANIC ANION TRANSPORT PROTEIN 1.
                          SLC22A6 OR OAT1 OR ROAT1.
Homo sapiens (Human).
              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic structure and in Vivo expression of the human organic anion transporter 1 (hOAT1) gene.";
Biochem. Biophys. Res. Commun. 275:623-630(2000).
EMBL; AJ271205; CAB97249.1;
EMBL; AJ271205; CAB97249.1;
E1748C6F9E2002F2 CRC64;
                                                                                                                                                                                                                                                                                    193 KVARTINGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFL 248
                                                                                                                                                                                                                                                  290 RVARINGKREEGAKLSMEVLRASIQKELIMGKGQASAMELLRCPTLRHLFLCLSML 345
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                                                                                                                                                                                                                                                                                                                                                                                                 170 LQTAVSGTCAAFAPNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPIHTRACVGTLIGYV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9NQA6 PRELIMINARY; PRT; 519 AA.
Q9NQA6;
Q1-QCT-2000 (Trembirel 15, Created)
Q1-QCT-2000 (Trembirel 15, Last sequence update)
Q1-DEC-2001 (Trembirel 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 IYDNSTFPSTIVTEWDLVCSHRALRQLAQSLYMVGVLLGAMVFGYLADRLGRRKVLILNY 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20422308; PubMed=10964714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 AN----LSKNGGLEVWLPRDRQGQPESCLRFTSPQWGLPFLNGT-EANGTGATEPCTDGW 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPOWQLLHLNGTIHSTSEADTEPCVDGW 120
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Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.6%; Score 458.5; DB 4; Length 519; 29.2%; Pred. No. 6.3e-36; ative 51; Mismatches 82; Indels 119
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SEQUENCE FROM N.A.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ORGANIC ANION TRANSPORTER 4 (OAT4)
HOAT4 OR OAT4.
Rowen L., Madan A., Qin S., Baradarani L., Birditt B., I Burke J., Dors M., Fleetwood P., Kaur A., Madan A., Nesl Pate D., Hood L.;
"Sequencing of human neurexin II gene.";
submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB026116; BAA95316.1;
EMBL; AC044790; AAK68155.1;
EMBL; AC044790; AAK68155.1;
SEQUENCE 550 AA; 59971 MW; 233BE6C4A520E58A CRC64;
                                                                                                                                                                                                                                                                                                                       Cha S.H., Sekine T., Kusuhara H., Yu E., Kim J.Y., Kim D.K., Sugiyama Y., Kanai Y., Endou H.; Sugiyama Y., Kanai Y., Endou H.; "Molecular cloning and characterization of multispecific organic anion transporter 4 expressed in the placenta."; J. Biol. Chem. 275:4507-4512(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20127945; PubMed=10660625;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 FSFGHGLTAAVAYGVRDWTLLQLVVSVPFFLCFLYSWWLAESARWLLTTGRLDWGLQELW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LQMAVMGTAAAFAPAFPVYCLFRFLLAFAVAGVMMNTGTLLMEWTAARARPLVMTLNSLG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASTLGSLSPEALLAISIPPGPNQRPHQCRRFRQPQWQLLDPNATATSWSEADTEPCVDGW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAFSELLDLVGGLGRFQVLQTMALMVSIMWLCTQSMLENFSAAVPSHRCWAPLLDNSTAQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVAAINGKGAVQDTLTPEVLLSAMREELSMGQPPASLGTLLRMPGLRFRTCI 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qin S., Baradarani L., Birditt B., Bloom S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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37.8%; Pred. No. 1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         550 AA
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                                                                                                                                                                                                                                                  Birditt B., Bloom S.,
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                                                                                                                                                                                                                        Nesbitt
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                                                                                                                                                                                                                                                                                                                    ALD DE RECORDE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                         밁
                                                                                                            QY
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                                                                                                                                                                         Matches 120;
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mori K., Ogawa Y., Ebihara K., Aoki T., Tamura N., Sugawara A., Kuwahara T., Ozaki S., Mukoyama M., Tashiro K., Tanaka I., Nakao K.; "Kidney-specific expression of a novel mouse organic cation transporter-like protein."; FEBS Lett. 417:371-374(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 CCLQLAVAGTSTIFAPTFVIYCGLRFVAAFGMAGIFLSSLTLMVEWTTTSRRAVTMTVVG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                       Transmembrane SEQUENCE 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98072412; PubMed=9409754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 LRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 CAFSAGQAALGGLAFALRDWRTLQLAASVPFFAISLISWWLPESARWLIIKGKPDQALQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAFSKLLEQAGGVGLEQTLQVLTFILPCLM--IPSQMLLENESAAIPGHRCWTHMLDN--
                                                                                                                                                                                                          Local Similarity
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                                                                                                            1 MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GWYYDQSYFPSTIVTKWDLYCDYQSLKSVVQFLLLTGMLYGGIIGGHVSDR------ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSAVSTN-MTPKALLTISIPPGPNQGPHQCRRFRQPQWQLLDPNATATSWSEADTEPCVD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVD 118
GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                      MAFPELLDRYGGLGRFQLFQTVALYTPILMYTTQNMLENFSAAVPHHRCWYPLLDNSTSQ 60
                                                                                                                                                                                                                                                                                                                       553 AA; 60160 MW; D991F5F74A39BBBF CRC64;
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                                                                                                                                                                               Conservative
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                                                                                                                                                                                                          39.2%; Score 551; DB 11; Length 553; 34.1%; Pred. No. 7.3e-45;
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19,
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                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -WLVESARWLIITNKLDEGLKA 190
                                                                                                                                                                                           86;
                                                                                                                                                                                           Indels 108;
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                                                                                                                                                                                                 Gaps
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61 ASIPGDLGPDVLLAVSIPPGPDQQPHQCLRFRQPQWQLTESNATATNWSDAATEPCEDGW 120

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RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA Matsumota Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,
RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Satoh H., Ota T.,
RA Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K.,
RA Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K.,
RA Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
RA Kanehori K., Takahashi-Tujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Kanehori K., Takahashi-Tujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
SQ SEQUENCE 552 AA; 62140 MW; 39A831COFD26CA68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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01-DEC-2001 (TremBirel. 19, Last sequence update)
01-DEC-2001 (TremBirel. 19, Last annotation update)
01-DEC-2001 (TremBirel. 19, Last annotation update)
CDNA FLJ33092 FIS, CLONE TRACH2000665, MODERATELY SIMILAR TO RATTUS
NORVEGICUS PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN (USTIR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                          169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96LX3;
181 LQFAITETCVAFAPSFFIYCLLRFLAGMSVEPISVNSHLLMLEWTSPKFLGMVAVLTSCA 240
                                                                                                                            121 VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSD------ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suzuki O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 KVARTNGIKNAEETLNIEVVRSTMOEELDAAQTKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                       61 DNGSRILSQDDLLRISIPLDSNLRLDKCRRFAQPQWHLLHLNGTFSNETEPDTEPCVDGW 120
                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                    Match 55.0%; Score 773; DB 4; Local Similarity 43.4%; Pred. No. 2.2e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                              1 MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                        MAFQELLNQVGSLGRFQILQISFVLFLVGLVVPHITMENFTAAIPNHRCWAPILDNDTAS 60
                                                                                     VYDRSNFLSTIVTEWDLVCESQALNSVAKFSFMIGLFIGAIICGHLSDRFGRKFILTCAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAIGQTVLAGLAFTVRNWHHLHLAMSVPIFFLLVPTRWLSESARWLIMTNKLQKGLKELI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----RWLVESARWLIITNKLDEGLKALR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQMAVTETCAAFAPTFLIYCSLRFLAGISFSTVLTNSALLIIEWTRPKFQALATGLLLCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYDQSTFLSTIITEWDLVCESQSLDSIAKFLFLTGILVGNILYGPLTDRFGRRLILICAS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSD----- 168
                                                                                                                                                                                                                                                                                                                                                         155;
                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               552 AA
                                                                                                                                                                                                                                                                                                                                              53; Indels 108;
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RESULT Q96S37 ID Q96S37 O9 O9 OT O11 DT O11 DT O11 DT O1 DT RS OS HC OC Eu OC Ma
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Q91WJ2
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Best Local
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                                                                                 Q96S37;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                         RST
                                                  Homo sapiens (Human)
                                                                                                                                                                  Q96S37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC014805; AAH14805.1; -. SEQUENCE 552 AA; 61360 MW; F5D2498FC673E8FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TremBLrel. 19, Created)
01-DEC-2001 (TremBLrel. 19, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
SIMILAR TO SOLUTE CARRIER FAMILY 22 (ORGANIC CATION TRANSPORTER)-LIKE
                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                      193 KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                                                                                                                                                                                                                                              181 LQMAITGTCTALAPTFFIYCLLRFLTGLCIIPINTNSVLLMLEWTSPKTQALVTTLSMSS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                      241 HHFGGLILAGLAFAFQNWHHLQLAISVPIFVLLIPTRWLTESARWLIVTNKPQKALQELR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSD------ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VYDQRTFLSTTVTEWNLVCGSQELNSVAKFIFLIGVLAGHFVGGHLSDKFGRKLLFRCAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 KVAHMNGMKNSGNTLTMEVVEASMKNELEAAKRKSSPRDLFHTPILRKRICVLSFMR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NNNSGILSQDDLLRISIPLDSNLRPEKCRRFVQPQWHLLQFNGSFSNMTEPDTEPCMDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GNETGILSEDALLRISIPLDSNLRÞEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ASIGYMILAGLAFLFRIWRHLQLAMSVPIFFFLILTRWMSESARWLIVTNKPQKGLKELR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 53.4%; Local Similarity 41.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAFQDLLNLVGSHGRFQILQMAFLLICNVITMPHVILENFTAANLGHRCWVHIIDNDTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAFFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                   KVASKNGIKNSEDVLTMEVVRTIMKDEIAIPRTKPSLRDLFHMPNLRKRLCLLCLLR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Mismatches
                                                                                                      Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 751; DB 1
Pred. No. 3e-64;
                                                                                  Last annotation update)
               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F5D2498FC673E8FC CRC64;
                                                                                                                                                                                                                                                                                                                                                             -----RWLVESARWLIITNKLDEGLKALR 192
                                                                                                                                                              553 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Result
No.
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                             pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 458.5
458.5
458.5
449.5
449.5
439.5
390.5
372.5
                                                                                                                                                                                                      Score
                                                                                                                                 818
773
751
601
592
                                                                                                                                                                                                       Match
                                                                                                                                                                                                                   Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        July 1, 2002, 11:39:10 ; Search time 26.48 Seconds (without alignments) 1750.855 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPTREMBL_19:*
1: sp_archea:
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAFEELLSQVGGLGRFQMLH.....RKKISRKRHKNDCYTKVTKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-674-235-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                           sp_phage: *
                                                                                                                                                                                                                                                                                                                                                                                                                   sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_mammai:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_fungi:*
                                                                                                                                                                                                                                                                                                             sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                   sp_unclassified:*
sp_rvirus:*
                                                                                                                                                                                                                                                                                                                                                                     sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                              sp_plant:*
                                                                                                                                                                                                                                                                                                                                                            sp_vertebrate: *
                                                                                                                                                                                                        Length
                                                         550
553
563
551
                                                                                                                                                                                                        DB
                                              Q9TSY7
Q9TSY7
057379
Q96TC1
Q96DT2
Q91WJ9
                                                                                               Q9NQC2
                                                                                                                                                                     Q96LX3
                                                                                                                                  Q9NSA0
                                                                                                                                                096837
                                                                                  095742
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                                                                                                                                                                                  070609
                                     Q61185
                                                                                                                     054778
                                                                                                                                                                                                                                           SUMMARIES
           O9tsy7 oryctolagus
O57379 pseudopleur
O61185 mus musculu
O96tc1 homo sapien
O96dt2 homo sapien
                                                                                                                     Q91wj2 mus musculu
Q96s37 homo sapien
Q9nsa0 homo sapien
Q9nsa0 mus musculu
                                                                                              Q9nqc2 homo sapien
Q9nqa6 homo sapien
                                                                                                                                                                      Q961x3 homo
                                                                                                                                                                                                        Description
                                                                                  095742 homo sapien
                                                                                                                                                                      070609 rattus norv
1961x3 homo sapien
                                                                        035956 rattus norv
   mus
   musculu
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	178.5	179.5	179.5	182.5	184	189.5	190.5	190.5	191.5	192	192.5	197.5	197.5	197.5	202.5	220	223	223	228	228	234	296.5	306	307.5	312.5	318	324.5	362.5	367.5
																												25.8	
	551	557	551	502	177	577	557	555	567	370	567	576	568	553	553	564	548	548	604	538	551	548	568	539	140	540	535	536	537
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	014546	Q9VEX8	Q9H015	Q9V8Z3	Q96ER0	Q96RU0	Q96EH6	Q961R9	Q9VCA3	001383	Q95R48	002270	Q9U539	Q9Z306	Q9R141	Q9WTN6	Q9VCA2	001384	Q961J5	Q9V6H5	Q9Y226	Q9Y694	095820	Q9H2W5	Q9QYA0	Q91WU2	Q63314	Q9R1U7	088909
	O14546 homo sapien		Q9h015 homo sapien			nomo	homo	Q96lr9 drosophila			Q95r48 drosophila	002270 caenorhabdi		·	rat		0		Q961j5 drosophila	Q9v6n5 drosopnila	Q9y226 homo sapien	nomo	homo	nomo	o ratt	2 mus mus	ract	rattus	mus mus

ALIGNMENTS

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RESULT
070609
                                                                                                                                                                                                                                                                                                                                                                                          SOUTH THE SECTION OF 
                                   Š
                                                                                                                                    Query Match 58.2%; Score 818; DB 11; Best Local Similarity 45.9%; Pred. No. 9.5e-71; Matches 164; Conservative 40; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O70609 PRELIMINARY; PRT; 552 AA. 070609; 01-AUG-1998 (TrEMBLrel. 07, Created) 01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY -:- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. EMBL; Y09945; CAA71076.1; -. Interpro; IPR003662; sub_transporter. PF00083; sugar_tr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98200080; PubMed=9541011;
Schoemig E., Spitzenberger F., Engelhardt M., Martel F., Oerding N.,
                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane.
SEQUENCE 552 AA; 61476 MW; F47FB42B41F5C4AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning and characterization of two novel transport proteins from rat kidney."; FEBS Lett. 425:79-86(1998).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gruendemann D.;
MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                                                                         45;
                                                                                                                                                                                                                                           Length 552;
                                                                                                                                                         Indels 108;
                                                                                                                                                         Gaps
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B

MAFQDLLNQVGSLGRFQILQMTFILIFNIIISPHSLLENFTAVIPNHRCWVPILDNDTVS 60